

GenCore version 5.1.6
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MM protein - protein search, using sw model

run on: November 21, 2003, 15:19:18 ; Search time 58.8082 Seconds

(without alignments)

286.100 Million cell updates/sec

title: US-09-010-377-1
effect score: 562
sequence: 1 DIQMTQSPSSLSSAVGDRVT.....YCLQYDNLWTFQGQTKWEIK 106

coring table: BLOSUM62
GapP 10.0 , Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters:

1107863

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

database : A_Geneseq_19Jun03; *
1: - /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1980.DAT; *
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3: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1982.DAT; *
4: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1983.DAT; *
5: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1984.DAT; *
6: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1985.DAT; *
7: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1986.DAT; *
8: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1987.DAT; *
9: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1988.DAT; *
10: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1989.DAT; *
11: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1990.DAT; *
12: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1991.DAT; *
13: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1992.DAT; *
14: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1993.DAT; *
15: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1994.DAT; *
16: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1995.DAT; *
17: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1996.DAT; *
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19: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1998.DAT; *
20: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA1999.DAT; *
21: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA2000.DAT; *
22: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA2001.DAT; *
23: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA2002.DAT; *
24: /SIDS1/gcdata/geneseq/geneseq/geneseqp-emb1/AA2003.DAT; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

SUMMARIES

result No.	Score	Query	Match	Length	DB ID	Description
1	562	100.0	106	16	AA81321	Humanized anti-VLA
2	562	100.0	106	18	AAW2412	Humanised alpha-4
3	562	100.0	126	18	AAW2419	Humanised alpha-4
4	508	90.4	106	16	AA81328	Mouse anti-VLA-4 a
5	508	90.4	126	16	AA81326	Mouse VLA-4 antabo
6	508	90.4	126	16	AA81332	Human VLA-4 reshaf
7	488	86.8	126	18	AAW2409	Alpha-4 integrin m
8	488	86.8	359	20	AAV29913	Human MCP-3 and mu
9	488	86.8	361	20	AAV29911	Human IP-10 and mu

10	488	86.8	374	20	AY29916
11	481	85.6	128	15	AAR0627
12	475.5	84.6	234	12	AAR13050
13	471.5	83.9	107	16	AAR78970
14	465	82.7	108	17	AAR91579
15	460.5	81.9	128	11	AAR06252
16	460	81.9	637	18	AAR26783
17	456	81.1	109	19	AAR26797
18	455	81.0	240	16	AAR85495
19	455	81.0	241	13	AY21882
20	455	81.0	245	19	AAW28800
21	453.5	80.7	107	16	AAR81322
22	453.5	80.7	107	18	AAW2422
23	453	80.6	109	12	AAR13658
24	452	80.4	241	13	AAR26981
25	451.5	80.3	108	16	AAR65163
26	451.5	80.3	129	15	AAR4207
27	451	80.2	355	18	AAW35133
28	449.5	80.0	107	19	AAR70625
29	449.5	80.0	107	23	ABP61194
30	449.5	80.0	107	23	ABP61241
31	446.5	79.4	108	18	AAR10231
32	446.5	79.4	110	19	AAW70673
33	446.5	79.4	110	23	ABP61242
34	446.5	79.4	234	18	AAB62087
35	446.5	79.4	237	19	AAB70703
36	446.5	79.4	650	23	ABP61241
37	445.5	79.3	107	19	AAW8684
38	445.5	79.3	107	19	AAW70623
39	445.5	79.3	107	23	ABP61192
40	445	79.1	107	20	AAB87455
41	444.5	79.1	107	22	AAB62087
42	444.5	79.1	107	22	AAB61400
43	444.5	79.1	107	22	AAB61585
44	444.5	79.1	108	19	AAW70622
45	444.5	79.1	108	21	AY82345

ALIGNMENTS

RESULT 1	AAW81321	02-APR-1996 (first entry)
ID	AAR81321	standard; Protein; 106 AA.
XX	AC	AAR81121;
XX	XX	02-APR-1996 (first entry)
XX	DT	Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX	DE	Humanized anti-VLA-4 leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.
XX	XX	Human antibody; leukocyte engineering.
XX	XX	Chimeric Muus musculus.
OS	OS	Chimeric Homo sapiens.
XX	PN	W09519790-A1.
XX	XX	27-JUL-1995.
PD	PP	25-JAN-1995;
XX	XX	95WO-US0186249.
PR	PR	25-JAN-1994;
XX	XX	94US-0186249.
PA	PA	(ATH-E) ATHENA NEUROSCIENCES INC.
XX	XX	Bendig MM, Jones TS, Leger OJ, Saldanha J;
PI	PI	WPI; 1995-229276/35.
XX	XX	New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating

inflammatory disease.

Claim 9; Page 67; 105pp; English.

The sequence encodes the humanized mouse antibody 21.6 light chain variable region, La, directed against leukocyte adhesion molecule VLA-4. Cloned cDNAs sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and I69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 IgL chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.

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sequence 106 AA;

st Local Similarity	100.0%	Pred. No.	1-4e-36
Matches	106	Mismatches	0
Indels	0	Gaps	0
1	DIQMTQSPSSLSASVGDRVTITCKTSQDINKMWNQQTPGKAPRLLIHTYSAQLPGIPS	60	
1	DIQMTQSPSSLSASVGDRVTITCKTSQDINKMWNQQTPGKAPRLLIHTYSAQLPGIPS	60	
61	RFSGSGSGRDYTFITSSLOPEDIATYCYLQYDINWTFGGTGVIEK 106		
61	RFSGSGSGRDYTFITSSLOPEDIATYCYLQYDINWTFGGTGVIEK 106		

01 KFSGSGSGKRLISSLQFSDRIL
LT 2
2412 AA22412 standard: Protein: 106 AA.

AAW22412; 08-DEC-1997 (first entry)
Humanised alpha-4 integrin antibody 21.6 VL La.

Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.

Chimeric *Mus musculus*;
Chimeric *Homo sapiens*;
Chimeric synthetic.

Key Region Location/Qualifiers
1:23 /label= FR1
 /note= "REI framework region 1"

Region 24..34 /label= CDR1 /note= "21.6 complementarity determining region 1
 Region 35..49 /label= FR2 /note= "REI framework region 2"
 Misc-difference 45 /note= "REI Lys-45 is substđ. by Lys of mouse 21.6 VL, important in supporting the

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protein - protein search, using sw model

on: November 21, 2003, 15:21:54 ; Search time 19.9658 Seconds
(without alignments)
224.622 Million cell updates/sec

le: US-09-010-377-1
fect score: 562
uence: 1 DIQMTQSPSSLSASVGDRVT..... YCLQYDNLNTFGQGTKEIK 106

ring table: BL03M62
Gapop 10.0 , Gapext 0.5
rched: 328717 seqs, 42310858 residues

al number of hits satisfying chosen parameters: 328717

minimum DB seq length: 0
minimum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:
* 6:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	562	100.0	2 US-08-561-521-7	Sequence 7, Appli
2	562	100.0	5 PCT-US93-01219-7	Sequence 7, Appli
3	508	90.4	5 US-08-561-521-5	Sequence 5, Appli
4	508	90.4	5 PCT-US95-01219-5	Sequence 5, Appli
5	508	90.4	2 US-08-561-521-2	Sequence 2, Appli
6	508	90.4	2 US-08-561-521-15	Sequence 2, Appli
7	508	90.4	126 PCT-US95-01219-2	Sequence 2, Appli
8	508	90.4	126 5 PCT-US95-01219-15	Sequence 15, Appli
9	488	86.8	359 4 US-09-646-028-16	Sequence 16, Appli
10	488	86.8	361 4 US-09-646-028-13	Sequence 13, Appli
11	488	86.8	374 4 US-09-646-028-15	Sequence 15, Appli
12	481	85.6	128 1 US-08-838-366-22	Sequence 4, Appli
13	471.5	83.9	107 2 US-08-838-366-22	Sequence 22, Appli
14	460	81.9	637 1 US-08-225-838-16	Sequence 16, Appli
15	460	81.9	637 2 US-08-445-473B-16	Sequence 16, Appli
16	455	81.0	241 1 US-08-235-838-11	Sequence 11, Appli
17	455	81.0	241 2 US-08-465-473B-11	Sequence 11, Appli
18	454.5	80.9	108 2 US-08-602-725-29	Sequence 29, Appli
19	453.5	80.7	107 2 US-08-561-521-8	Sequence 8, Appli
20	453.5	80.7	107 5 PCT-US95-01219-8	Sequence 8, Appli
21	451	80.2	355 3 US-08-875-811-57	Sequence 57, Appli
22	448.5	79.8	107 2 US-07-934-71C-17	Sequence 17, Appli
23	448.5	79.8	107 3 US-08-436-642B-17	Sequence 17, Appli
24	448.5	79.8	107 4 US-08-146-208C-17	Sequence 17, Appli
25	448.5	79.8	107 5 PCT-US93-07832-17	Sequence 17, Appli
26	444.5	79.1	107 2 US-07-934-371C-18	Sequence 18, Appli
27	444.5	79.1	107 3 US-08-437-642B-18	Sequence 18, Appli

ALIGNMENTS

RESULT: 1
US-08-561-521-7
Sequence 7, Application US/08561521
Patent No. 5940299
GENERAL INFORMATION:
APPLICANT: BendiG, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.25
CURRENT APPLICATION DATA: US/08/561-521
APPLICATION NUMBER: US/08/561-521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186-269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-5043
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-7
Query Match Score 100.0%; DB 2; Length 106;
Best Local Similarity 100.0%; Prod. No. 1.0e-45;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
CT-US95-01219-7

GENERAL INFORMATION:

APPLICATION: Bendig, Mary M.

APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/561,521

FILING DATE: 08/08/1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:

APPLICATION NUMBER: PCT/US95/01219

FILING DATE: 25-JAN-1995

CLASSIFICATION:

APPLICATION NUMBER: US 08/186,269

FILING DATE: 25-JAN-1994

CLASSIFICATION:

APPLICATION NUMBER: 30,223

REGISTRATION NUMBER:

NAME: Smith, William L.

TELECOMMUNICATION INFORMATION:

TELEFAX: 415-543-9600

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-561-521-5

Query Match 90.4%; Score 508; DB 2; Length 106;

Best Local Similarity 88.7%; Pred. No. 1.7e-40; Indels 0; Gaps 0;

Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db 1 DIQMTOQSPSSIASVGDRVTICKTSQDINKYMAWYQQTGKAPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDTYTFISSLQPEDIATYYCLQYDNLWTFGQGTIVK 106

Db 61 RFSGSGSGRDTYTFISSLQPEDIATYYCLQYDNLWTFGQGTIVK 106

RESULT 4
PCT-US95-01219-5

Sequence 5, Application PC/CTUS95-01219

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

RESULT 3
S-08-261-521-5

Sequence 5, Application US/08561521

Patent No. 5840299

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M protein - protein search, using sw model

run on: November 21, 2003, 15:27:54 ; Search time 39.5685 Seconds

(without alignments)
489.058 Million cell updates/sec

Perfect score: 562

Sequence: 1 DIQMTQSPSSLSASVGDRVTI...YCLQYDNLWTGGTKEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:^{*}

1: /cgn2_6/ptodata/1/pubpaa/us07_pubcomb.pep:
2: /cgn2_6/ptodata/1/pubpaa/pc07_new_pub.pep:
3: /cgn2_6/ptodata/1/pubpaa/us06_pub.pep:
4: /cgn2_6/ptodata/1/pubpaa/us07_new_pub.pep:
5: /cgn2_6/ptodata/1/pubpaa/us07_pub.pep:
6: /cgn2_6/ptodata/1/pubpaa/pc05_pubcomb.pep:
7: /cgn2_6/ptodata/1/pubpaa/us08_new_pub.pep:
8: /cgn2_6/ptodata/1/pubpaa/us08_pubcomb.pep:
9: /cgn2_6/ptodata/1/pubpaa/us09_pubcomb.pep:
10: /cgn2_6/ptodata/1/pubpaa/us06_pubcomb.pep:
11: /cgn2_6/ptodata/1/pubpaa/us09c_pubcomb.pep:
12: /cgn2_6/ptodata/1/pubpaa/us09_new_pub.pep:
13: /cgn2_6/ptodata/1/pubpaa/us08_pubcomb.pep:
14: /cgn2_6/ptodata/1/pubpaa/us10b_pubcomb.pep:
15: /cgn2_6/ptodata/1/pubpaa/us10c_pubcomb.pep:
16: /cgn2_6/ptodata/1/pubpaa/us10_new_pub.pep:
17: /cgn2_6/ptodata/1/pubpaa/us06_new_pub.pep:
18: /cgn2_6/ptodata/1/pubpaa/us00_pubcomb.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB ID	Description
1	498	86.8	359	12	US-10-335-394-16	Sequence 16, Appl.
2	488	86.8	361	12	US-10-335-394-13	Sequence 13, Appl.
3	488	86.8	374	12	US-10-335-394-15	Sequence 15, Appl.
4	479.5	85.3	108	9	US-09-229-200A-11	Sequence 11, Appl.
5	479.5	85.3	108	9	US-09-229-200A-15	Sequence 15, Appl.
6	466.5	83.0	108	9	US-09-229-200A-16	Sequence 16, Appl.
7	449.5	80.0	107	9	US-09-056-160B-15	Sequence 15, Appl.
8	449.5	80.0	107	12	US-10-34-671-15	Sequence 15, Appl.
9	446.5	79.4	110	12	US-09-056-160B-103	Sequence 103, Appl.
10	446.5	79.4	110	12	US-10-234-671-101	Sequence 101, Appl.
11	446.5	79.4	237	9	US-09-056-160B-100	Sequence 100, Appl.
12	446.5	79.4	237	12	US-10-234-671-100	Sequence 100, Appl.
13	446.5	79.4	491	14	US-10-011-125-2	Sequence 2, Appl.
14	445.5	79.3	107	9	US-09-160B-13	Sequence 13, Appl.
15	445.5	79.3	107	12	US-10-234-671-13	Sequence 13, Appl.

RESULT 1
US-10-335-394-16
; Sequence 16, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwaik, Larry
; BIRAGYAN, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014-0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 359

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence :/note=synthetic construct
US-10-335-394-16
Query Match 86.8%; Score 488; DB 12; Length 359;
Best Local Similarity 84.9%; Pred. No. 6 8e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 D1QMTQSPSSLSASVGDRVTIITCKTSQDINKYAWQQTGKAPRLIHTYTSALQPGIPS 60
Db 233 D1QMTQSPSSLSASVGDRVTIITCKTSQDINKYAWQQTGKAPRLIHTYTSALQPGIPS 292
Qy 61 RPSGSGSGRDTYPTFISQLEPDITYTICQYDNLWTFGOTKRIK 106
Db 293 RPSGSGSGRDTYPTFISQLEPDITYTICQYDNLWTFGOTKRIK 338

RESULT 2
 US-10-335-394-13
 ; Sequence 13, Application US/10335394
 ; GENERAL INFORMATION:
 ; APPLICANT: Bragyn, Arya
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
 ; CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
 ; FILE REFERENCE: 14014_0316/P
 ; CURRENT APPLICATION NUMBER: US/10/335,394
 ; CURRENT FILING DATE: 2002-12-31
 ; PRIORITY NUMBER: US/09/646,028
 ; PRIORITY FILING DATE: 2000-09-12
 ; PRIORITY APPLICATION NUMBER: 60/077,745
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; LENGTH: 361
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
 US-10-335-394-13

Query Match 86.8%; Score 488; DB 12; Length 361;
 Best Local Similarity 84.9%; Pred. No. 6.e-37;
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
 Db 235 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 294

Qy 61 RFSGSGSGRDRYTFITSIQPEDATYCLQDNLWTFGGTKEIK 106
 Db 295 RFSGSGSGRDRYTFISIQLNLYTFGGTKEIK 340

RESULT 3
 US-10-335-394-15
 ; Sequence 15, Application US/10335394
 ; GENERAL INFORMATION:
 ; APPLICANT: Kwak, Larry
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
 ; CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
 ; FILE REFERENCE: 14014_0316/P
 ; CURRENT APPLICATION NUMBER: US/10/335,394
 ; CURRENT FILING DATE: 2002-12-31
 ; PRIORITY NUMBER: US/09/646,028
 ; PRIORITY FILING DATE: 2000-09-12
 ; PRIORITY APPLICATION NUMBER: 60/077,745
 ; PRIORITY FILING DATE: 1998-03-12
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
 US-10-335-394-15

Query Match 86.8%; Score 488; DB 12; Length 374;
 Best Local Similarity 84.9%; Pred. No. 7.1e-37;
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
 Db 95 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 154

RESULT 4
 US-09-229-200A-11
 ; Sequence 11, Application US/09229200A
 ; Patent No. US20020099179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jolliffe et al.
 ; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Johnson & Johnson
 ; STREET: One Johnson & Johnson Plaza
 ; CITY: New Brunswick
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08933-7003

Query Match 85.3%; Score 479.5; DB 9;
 Best Local Similarity 85.8%; Pred. No. 1.2e-36;
 Matches 91; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
 Db 1 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDRYTFITSIQPEDATYCLQDNLWTFGGTKEIK 105
 Db 61 RFSGSGSGRDRYTFITSIQPEDATYCLQDNLWTFGGTKEIK 106

RESULT 5
 US-09-229-200A-15
 ; Sequence 15, Application US/09229200A
 ; Patent No. US20020099179A1
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Johnson & Johnson
 ; STREET: One Johnson & Johnson Plaza
 ; CITY: New Brunswick
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08933-7003

Query Match 85.3%; Score 479.5; DB 9;
 Best Local Similarity 85.8%; Pred. No. 1.2e-36;
 Matches 91; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
 Db 1 D1QMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60

result	No.	Score	Query	Match	Length	DB	ID	Description
1	488	86.8	PIR:76.1*	S26330	104	2	S26330	Ig kappa chain V region
2	479	85.2	1: PIR:1.1*	S26329	104	2	S26329	Ig kappa chain V region
3	478	85.1	2: PIR:1.1*	S26329	105	2	S26329	Ig kappa chain V region
4	463.5	82.5	3: PIR:1.1*	S26329	125	2	S26329	Ig kappa chain V region
5	452	80.4	4: PIR:1.1*	S26329	97	2	S26329	Ig kappa chain V region
6	446.5	79.4	PL0270	S26329	107	2	S26329	Ig kappa chain V region
7	443.5	78.9	PL0270	S26329	108	1	S26329	Ig kappa chain V region
8	443	78.9	KLHURE	S26329	129	2	S26329	Ig kappa chain V region
9	443	78.8	PL0270	S26329	103	2	S26329	Ig kappa chain V region
10	440.5	78.4	PL0272	S26329	107	2	S26329	Ig kappa chain V region
11	440	78.3	PL0272	S26329	94	2	S26329	Ig kappa chain V region
12	439.5	78.2	PL0269	S26329	107	2	S26329	Ig kappa chain V region
13	439.5	78.2	PL0271	S26329	107	2	S26329	Ig kappa chain V region
14	439.5	78.2	PL0271	S26329	108	1	S26329	Ig kappa chain V region
15	435.5	77.5	PL0269	S26329	108	1	S26329	Ig kappa chain V region
16	429.5	76.4	PL0269	S26329	110	2	S26329	Ig kappa chain V region
17	429.5	76.4	PL0270	S26329	127	2	S26329	Ig kappa chain V region
18	426	75.8	PL0270	S26329	107	2	S26329	Ig kappa chain V region
19	424.5	75.5	PL0270	S26329	125	2	S26329	Ig kappa chain V region
20	421.5	75.0	PL0270	S26329	108	1	S26329	Ig kappa chain V region
21	419.5	74.6	PL0272	S26329	108	1	S26329	Ig kappa chain V region
22	419.5	74.6	PL0272	S26329	108	1	S26329	Ig kappa chain V region
23	415.5	74.5	PL0269	S26329	123	2	S26329	Ig kappa chain V region
24	415.5	73.9	PL0269	S26329	109	2	S26329	Ig kappa chain V region
25	414.5	73.8	PL0270	S26329	131	2	S26329	Ig kappa chain V region
26	413.5	73.7	PL0270	S26329	124	2	S26329	Ig kappa chain V region
27	412.5	73.6	PL0270	S26329	108	1	S26329	Ig kappa chain V region
28	412.5	73.4	PL0270	S26329	108	2	S26329	Ig kappa chain V region
29	412	73.3	PL0270	S26329	106	2	S26329	Ig kappa chain V region

RESULT 5

PH1064 Ig light chain V region (clone 202.54) - mouse (fragment)
 Ig light chain V region (clone 202.54) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Accession: PH1064
 C:Author: R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
 A:Reference number: PH0911; PMID:9238144; PMID:1512540
 A:Accession: PH1064
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-97 <URL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-50/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 452; DB 2; Length 97;
 Best Local Similarity 85.6%; Pred. No. 2e-32;
 Matches 83; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAKRPLIHYTSALQPGIPS 60
 Db 1 DIQMTQSPSSLSASLGKVTTCKASQDINKYIAWYQHKEPGKGPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDYTFITSSLQPEDIATYCYQDNWTF 97
 Db 61 RFSGSGSGRDYFSITSLNPEDIATYCYQDNWTF 97

RESULT 6

PL00270 Ig kappa chain V region (anti-DNA, 6G6V) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Accession: PL00270 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Author: R.Hlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 C:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation
 A:Reference number: PL00231; MUID:9011618; PMID:2104919
 A:Accession: PL00270
 A:Molecule type: mRNA
 A:Residues: 1-107 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Region: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-107/Region: framework 4

Query Match 79.4%; Score 446.5; DB 2; Length 107;
 Best Local Similarity 79.4%; Pred. No. 6.5e-32;
 Matches 85; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAKRPLIHYTSALQPGIPS 60
 Db 1 DIQMTQSPSSLSASLGKVTTCKASQDINKYIAWYQHKEPGKGPRLLIHYTSALQPGIPS 60

Qy 61 RFSGSGSGRDYTFITSSLQPEDIATYCYQDNWTFQGQKVEIK 106
 Db 61 RFSGSGSGRDYFSITSLNPEDIATYCYQDNWTFQGSGTKLEIK 107

RESULT 7

KIHRE

Database :	SwissProt_41:*				Description
Result No.	Score	Match	Length	DB ID	
1	443.5	78.9	108	1 KV10_HUMAN	P01607 homo sapien
2	439.5	78.2	108	1 KV1B_HUMAN	P01594 homo sapien
3	421.5	75.0	108	1 KV1M_HUMAN	P01605 homo sapien
4	419.5	74.6	108	1 KV1A_HUMAN	P01593 homo sapien
5	419.5	74.6	108	1 KV1P_HUMAN	P01608 homo sapien
6	419.5	74.6	108	1 KV1Y_HUMAN	P01662 homo sapien
7	413.5	73.6	108	1 KV1Q_HUMAN	P01609 homo sapien
8	409.5	72.9	129	1 KV1W_HUMAN	P01431 homo sapien
9	409	72.8	107	1 KV1D_HUMAN	P01596 homo sapien
10	408.5	72.7	108	1 KV1R_HUMAN	P01610 homo sapien
11	402.5	71.6	108	1 KV1H_HUMAN	P01600 homo sapien
12	397.5	70.7	108	1 KV1F_HUMAN	P01598 homo sapien
13	396.5	70.6	108	1 KV1V_HUMAN	P04430 homo sapien
14	390.5	69.5	108	1 KV1K_HUMAN	P01603 homo sapien
15	388.5	69.1	108	1 KV1E_HUMAN	P01597 homo sapien
16	386.5	68.8	108	1 KV1L_HUMAN	P01604 homo sapien
17	385.5	68.6	108	1 KV1N_HUMAN	P01606 homo sapien
18	384.5	68.4	108	1 KV1C_HUMAN	P01595 homo sapien
19	383.5	68.2	108	1 KV1G_HUMAN	P01599 homo sapien
20	383.5	68.2	129	1 KV1X_HUMAN	P04432 homo sapien
21	381.5	67.9	108	1 KV1S_HUMAN	P01614 homo sapien
22	376.5	67.0	134	1 KV4C_HUMAN	P01643 mus musculu
23	371.5	66.1	108	1 KV5J_HOUSE	P01612 homo sapien
24	368	65.5	117	1 KV1J_HUMAN	P01637 mus musculu
25	366.5	65.2	128	1 KV5E_MOUSE	P06313 homo sapien
26	365	64.9	133	1 KV4B_MOUSE	P01648 mus musculu
27	364.5	64.9	108	1 KV5N_MOUSE	P01647 mus musculu
28	363.5	64.7	108	1 KV1T_MOUSE	P01612 homo sapien
29	362	64.4	109	1 KV1T_MOUSE	P01601 homo sapien
30	362	64.4	117	1 KV1I_HUMAN	P01644 mus musculu
31	361.5	64.3	108	1 KV5K_MOUSE	P01646 mus musculu
32	359.5	64.0	108	1 KV5M_MOUSE	P01645 mus musculu
33	358.5	63.8	108	1 KV5L_MOUSE	

ALIGNMENTS

RESULT 1

KV10_HUMAN ID: KV10_HUMAN STANDARD; PRT: 108 AA.

AC: P01607; DT: 21-JUL-1986 (Rel. 01, Created)
DT: 21-JUL-1986 (Rel. 01, Last sequence update)
DT: 15-SEP-2003 (Rel. 42, Last annotation update)

DB: Ig kappa chain V-I region Rei.

OS: Homo sapiens (Human).

OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606; OX: [1]

RN: RN

RP: SEQUENCE.

RX: MEDLINE-76023758; PubMed=8093329;

RA: Palm W.; Hilschmann N.;

RT: The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";

RT: Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).

[2]

RP: X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX: MEDLINE-76039968; PubMed=118213;

RA: Epp O.; Latzman B.-E.; Schiffer M.; Huber R.; Palm W.;

RT: "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rei refined at 2.0-A resolution.";

RL: Biochemistry 14:943-952 (1975).

CC: -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1, 2) MARKER.

CC: -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

CC: PTR: A91663; K1HURE.

DR: DR

PDB: IRI1; 17-FEB-94.

PDB: IAS2; 12-NOV-97.

PDB: 1BW2; 29-DEC-99.

InterPro: IPRO003006; Ig_MHC.

InterPro: IPRO003556; Ig_V.

DR: DR

GO: GO:0005516; C: extracellular; NAS.

DR: DR

Pfam: PF00047; 19; 1.

SMART: SM00406; Ig_V; 1.

PROSITE: PS50835; Ig_LIKE; 1.

DR: DR

InterPro: IPR007110; Ig_Like.

DR: DR

KW: ImmunoGlobulin V region; Bence-Jones protein; 3D-structure.

DOMAIN: DOMAIN 1

DR: DR

34 COMPLEMENTARITY-DETERMINING-1.

DOMAIN: DOMAIN 2

DR: DR

49 COMPLEMENTARITY-DETERMINING-2.

DOMAIN: DOMAIN 50

56 COMPLEMENTARITY-DETERMINING-2.

DOMAIN: DOMAIN 57

88 FRAMEWORK-3.

DOMAIN: DOMAIN 89

97 FRAMEWORK-4.

DISULFID: DISULFID 23

88 STRAND 4

GenCore version 5.1.6
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DM protein - protein search, using sw model

un on: November 21, 2003, 15:19:18 i Search time 68.2397 Seconds
(without alignments)

288.100 Million cell updates/sec

Title: US-09-010-377-2

Perfect score: 655

Sequence: 1 QVQLVQSGAEVKKPGASVRY.....NYGYAMDYWGQTLVTVSS 123

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
ID AAR81323 standard; Protein; 123 AA.

1: AAR81323; DT 02-APR-1996 (first entry)
XX Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
DE Humanized VLA-4 antibody: leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.
KW antibody
KW engineering.
XX OS musculus.
XX PN WO9519790-A1.
XX PD 27-JUL-1995.
XX PR 25-JAN-1995; 95WO-US01219.
XX PR 25-JAN-1994; 94US-0186269.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	655	100.0	123	16	AAR81323		Humanized VLA-4 and Human VLA-4 reshaped
2	655	100.0	142	16	AAR81333		Humanised alpha-4
3	655	100.0	142	18	AAR82428		Humanised alpha-4
4	648	98.9	123	18	AAR82413		Mouse anti-VLA-4 a
5	552	84.3	123	16	AAR81330		Mouse VLA-4 antibody
6	544	83.1	140	16	AAR81327		Alpha-4 integrin m
7	544	83.1	140	18	AAR82410		Heavy chain variable
8	523.5	79.9	120	19	AAR84124		New humanised antibodies against VLA-4 - used for inhibiting
9	523.5	79.9	120	23	AAR79034		leukocyte adhesion to endothelial cells, partic. for treating
							inflammatory disease.

XX
Claim 11; Page 69; 105pp; English.
XX
The sequence encodes the mouse antibody 21.6 heavy chain variable
CCC region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CCDNAs sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ9892) regions
CC are linked to human constant regions in the construction of a humanized
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
modified using PCR primers (See AAQ99895-98) and then subcloned into
mammalian cell expression vectors containing human kappa or gamma-1
constant regions. In the humanized light chain, amino acids L45,
L49, L58 and L69 in the human kappa LC VR framework are replaced
by the amino acid present in the equivalent position of the mouse
21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
transfected into COS cells. The humanized antibodies can be used
for inhibiting adhesion of a leukocyte to an endothelial cell and
treating inflammatory diseases such as multiple sclerosis. They
can also be used in the treatment of stroke, cerebral traumas,
meningitis or encephalitis. The antibodies can also be used for
detecting VLA-4, for affinity purification or for generating
anti-idiotype antibodies.

XX
Sequence 123 AA;
ISQ 100.0%; Score 655; DB 16; Length 123;
Query Match Best Local Similarity 100.0%; Pred. No. 7.2e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLYSGAELYKKPGASVYKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db 1 QVQLYSGAELYKKPGASVYKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
QY 61 DPKFQGRVITIADTSASTAAMELSSRLSEDTAVYTCAREGYGNVYAMDYNGQGTLYT 120
Db 61 DPKFQGRVITIADTSASTAAMELSSRLSEDTAVYTCAREGYGNVYAMDYNGQGTLYT 120
QY 121 VSS 123
Db 121 VSS 123

RESULT 2
AAR81333
ID AAR81333 standard; Protein; 142 AA.
XX
AC AAR81333;
XX
DT 23-MAR-1996 (first entry)
XX
Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
DE Humanised antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
Peptide 1..19
/note= "signal peptide"
FT Region 20..49
/note= "framework region 1"
FT Region 50..54
/note= "complementarity determining region 1"
FT Region 55..68
/note= "framework region 2"
FT Region 69..85
/note= "complementarity determining region 2"
FT Region 86..117
/note= "framework region 3"
FT Region 118..131
/note= "complementarity determining region 3"
FT Region 132..142
/note= "framework region 4"
FT Region

XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
(ATHB-) ATHENA NEUROSCIENCES INC.
PA
Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
WPI; 1995-269276/35.
XX
New humanised antibodies against VLA-4 - used for inhibiting
leukocyte adhesion to endothelial cells, partic. for treating
inflammatory disease.
XX
Disclosure; Fig 11; 105pp; English.
XX
The sequence represents the human reshaped antibody 21.6 heavy
chain variable region against leukocyte adhesion molecule VLA-4.
CC
Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ98989).
CC
Regions are linked to human constant regions in the construction
of a humanized antibody against VLA-4. The 5' and 3' ends of the
mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
subcloned into mammalian cell expression vectors containing human
kappa or gamma-1 constant regions. In the humanized heavy
chain, amino acids H27, H28, H30, H44 and H71 in the human HC VR
framework are replaced by the amino acid present in the equivalent
position of the mouse 21.6 Ig H chain. Plasmids encoding the
chimeric antibodies are transfected into COS cells. The humanized
antibodies can be used to inhibit adhesion of a leukocyte to an
endothelial cell and to treat inflammatory diseases such as multiple
sclerosis. They can also be used in the treatment of stroke,
cerebral traumas, meningitis or encephalitis. The antibodies can
also be used for detecting VLA-4, for affinity purification or for
generating anti-idiotype antibodies.
XX
Sequence 142 AA;
SQ Query Match 100.0%; Score 655; DB 16; Length 142;
Best Local Similarity 100.0%; Pred. No. 8.4e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLYSGAELYKKPGASVYKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
Db 20 QVQLYSGAELYKKPGASVYKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79
QY 61 DPKFQGRVITIADTSASTAAMELSSRLSEDTAVYTCAREGYGNVYAMDYNGQGTLYT 120
Db 80 DPKFQGRVITIADTSASTAAMELSSRLSEDTAVYTCAREGYGNVYAMDYNGQGTLYT 139
QY 121 VSS 123
Db 140 VSS 142

RESULT 3
AAW22428
ID AAW22428 standard; Protein; 142 AA.
XX
AC AAW22428;
XX
DT 09-DEC-1997 (first entry)
XX
Humanised alpha-4 integrin antibody 21.6 VL version Ha.
DE
XX
AAW22428;
XX
ID AAW22428
XX
DE Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
asthma; atherosclerosis; AIDS; dementia; tumour;
metastasis; inflammatory bowel disease; rheumatoid arthritis;

GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.

Copyright - protein search, using sw model

un on: November 21, 2003, 15:21:54 ; Search time 23.1678 Seconds
(without alignments)

224.632 Million cell updates/sec

title: US-09-010-377-2

effect score: 655

sequence: 1 QVQLVQSGAEVRKPGASVVKV.....NYGVYAMDYMGQGTLVTVSS 123

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 3,287,177 seqs, 423,10858 residues

total number of hits satisfying chosen parameters: 32,871,7

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

atabase : Issued Patents AA: *

1: /cgn2_6/ptodata/1/iaa/5A_COMBO.PEP: *
2: /cgn2_6/ptodata/1/iaa/5B_COMBO.PEP: *
3: /cgn2_6/ptodata/1/iaa/6A_COMBO.PEP: *
4: /cgn2_6/ptodata/1/iaa/6B_COMBO.PEP: *
5: /cgn2_6/ptodata/1/iaa/PC7US_COMBO.PEP: *
6: /cgn2_6/ptodata/1/iaa/backfile1.PEP: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	655	100.0	123	2	US-09-561-521-11		Sequence 11, App1
2	655	100.0	123	5	PCT-US95-01219-11		Sequence 11, App1
3	655	100.0	142	2	US-08-561-51-17		Sequence 17, App1
4	655	100.0	142	5	PCT-US95-01219-17		Sequence 17, App1
5	552	84.3	123	2	US-08-561-521-9		Sequence 9, App1
6	552	84.3	123	5	PCT-US95-01219-9		Sequence 9, App1
7	544	83.1	140	2	US-08-561-521-4		Sequence 4, App1
8	544	83.1	140	5	PCT-US95-01219-4		Sequence 4, App1
9	523	79.9	120	4	US-08-871-488A-19		Sequence 19, App1
10	523	79.8	117	3	US-08-646-265A-132		Sequence 13, App1
11	523	79.8	136	3	US-08-646-265A-99		Sequence 99, App1
12	523	79.8	269	3	US-08-646-265A-109		Sequence 109, App1
13	515	78.6	119	2	US-08-561-521-13		Sequence 13, App1
14	515	78.6	119	5	PCT-US95-01219-13		Sequence 13, App1
15	512	78.2	119	2	US-08-561-521-12		Sequence 12, App1
16	512	78.2	119	5	PCT-US95-01219-12		Sequence 12, App1
17	505	77.1	125	2	US-08-561-521-44		Sequence 44, App1
18	505	77.1	125	5	PCT-US95-01219-44		Sequence 44, App1
19	495	75.6	119	2	US-08-561-521-10		Sequence 10, App1
20	495	75.6	119	5	PCT-US95-01219-10		Sequence 10, App1
21	492	75.1	117	5	PCT-US95-10053-14		Sequence 17, App1
22	492	75.1	117	5	PCT-US95-01944B-17		Sequence 17, App1
23	492	75.1	117	5	PCT-US95-01219-44		Sequence 41, App1
24	492	75.1	119	4	US-09-438-141		Sequence 8, App1
25	491.5	75.0	118	2	US-08-232-181B-8		Sequence 36, App1
26	489.5	74.7	120	4	US-09-025-769B-36		Sequence 59, App1
27	489.5	74.7	120	4	US-09-025-769B-59		

ALIGNMENTS

28	486	74.2	140	3	US-09-836-561-63		Sequence 63, App1
29	486	74.2	140	4	US-09-434-12-63		Sequence 63, App1
30	484.5	74.0	135	1	US-08-137-11D-112		Sequence 112, App1
31	484.5	74.0	135	2	US-08-436-717-112		Sequence 112, App1
32	484.5	74.0	139	1	US-08-253-87C-19		Sequence 19, App1
33	484.5	74.0	139	3	US-08-552-16A-19		Sequence 19, App1
34	484.5	74.0	139	4	US-08-450-89-14		Sequence 14, App1
35	484.5	74.0	121	1	US-08-302-047-23		Sequence 23, App1
36	481	73.4	121	3	US-08-594-590-23		Sequence 23, App1
37	481	73.4	124	4	US-09-301-593-16		Sequence 16, App1
38	480.5	73.4	124	4	US-09-301-593-41		Sequence 41, App1
39	480.5	73.4	119	4	US-09-438-554-4		Sequence 4, App1
40	475	72.5	140	3	US-08-836-561-74		Sequence 74, App1
41	474	72.4	140	4	US-08-482-182-53		Sequence 53, App1
42	473	72.2	123	2	US-08-483-369-53		Sequence 53, App1
43	473	72.2	123	2	US-08-487-113D-53		Sequence 53, App1

QY 1 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 60
 Db 1 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 60

RESULT 3
 US-08-561-521-17
 Sequence 11, Application PC/TUS9501219
 GENERAL INFORMATION:
 APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Saldana, Jose
 APPLICANT: Jones, S. Tarran
 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 PATENT NUMBER: PCT/US95/01219
 FILING DATE: 25-JAN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/186,269
 FILING DATE: 25-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William L.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15270-14
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-543-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SBO ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 142 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-561-521-17

Query Match 100.0%; Score 655; DB 5; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-58;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-01219-11

QY 1 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 60
 Db 1 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 60

RESULT 4
 PCT-US55-01219-17
 Sequence 17, Application PC/TUS9501219
 GENERAL INFORMATION:
 APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Jones, S. Tarran
 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 PATENT NUMBER: PCT/US95/01219
 FILING DATE: 25-JAN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/186,269
 FILING DATE: 25-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William L.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15270-14
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-543-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SBO ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 142 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-561-521-17

Query Match 100.0%; Score 655; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-58;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 60
 Db 20 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 79

Qy 61 DPKFQGRVTITADTSASTAMELSSRLSRTDAVYYCAREGYGNVYANDYWQGTLYT 120
 Db 80 DPKFQGRVTITADTSASTAMELSSRLSRTDAVYYCAREGYGNVYANDYWQGTLYT 139

Query Match 100.0%; Score 655; DB 5; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-58;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-01219-11

Qy 1 QVQLVQSGAEEVKPGASVKSCKASGENIKDTYIHWVROAPGQLEWMGRIDPANGTYK 60
 Db 61 DPKFQGRVTITADTSASTAMELSSRLSRTDAVYYCAREGYGNVYANDYWQGTLYT 120
 Db 61 DPKFQGRVTITADTSASTAMELSSRLSRTDAVYYCAREGYGNVYANDYWQGTLYT 120

Qy 121 VSS 123
 Db 121 VSS 123

GenCore version 5.1.6
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Protein search, using sw model

Run on: November 21, 2003, 15:27:54 ; Search time 45.9144 Seconds

(without alignments)
489.058 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVSGAEGVKPGASVKV.....NYGYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs. 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6_ptodata/1/pubcaa/US07_PUBCOMB.pep:
2: /cgn2_6_ptodata/1/pubcaa/US07_PUBCOMB.pep:
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4: /cgn2_6_ptodata/1/pubcaa/US07_PUBCOMB.pep:
5: /cgn2_6_ptodata/1/pubcaa/US07_PUBCOMB.pep:
6: /cgn2_6_ptodata/1/pubcaa/PCUTUS_PUBCOMB.pep:
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9: /cgn2_6_ptodata/1/pubcaa/PUBCOMB.pep:
10: /cgn2_6_ptodata/1/pubcaa/US09C_PUBCOMB.pep:
11: /cgn2_6_ptodata/1/pubcaa/US09C_PUBCOMB.pep:
12: /cgn2_6_ptodata/1/pubcaa/US09__NEW_PUB.pep:
13: /cgn2_6_ptodata/1/pubcaa/US10A_PUBCOMB.pep:
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* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	523.5	79.9	120	15	US-10-056-794-19	Sequence 19, Appli
2	523.5	79.9	431	12	US-10-244-821-4	Sequence 4, Appli
3	523.5	79.9	431	15	US-10-013-173-4	Sequence 4, Appli
4	523.5	79.9	431	15	US-10-150-162-4	Sequence 4, Appli
5	523	79.8	117	11	US-09-749-873-132	Sequence 132, Appli
6	523	79.8	136	11	US-09-749-873-99	Sequence 99, Appli
7	523	79.8	269	11	US-09-749-873-109	Sequence 109, Appli
8	492	75.1	117	10	US-09-158-120A-17	Sequence 17, Appli
9	492	75.1	119	15	US-10-233-996-41	Sequence 11, Appli
10	491.5	75.0	245	11	US-09-880-748-896	Sequence 1896, Appli
11	486	74.2	140	15	US-10-283-349-63	Sequence 63, Appli
12	486	74.2	143	12	US-10-428-662-69	Sequence 69, Appli
13	485.5	74.1	120	14	US-10-025-687-2	Sequence 2, Appli
14	485.5	74.1	120	15	US-10-125-687-2	Sequence 2, Appli
15	484	73.9	180	9	US-09-748-960-6	Sequence 6, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	523.5	79.9	120	15	US-10-056-794-19	Sequence 19, Appli
2	523.5	79.9	431	12	US-10-244-821-4	Sequence 4, Appli
3	523.5	79.9	431	15	US-10-013-173-4	Sequence 4, Appli
4	523.5	79.9	431	15	US-10-150-162-4	Sequence 4, Appli
5	523	79.8	117	11	US-09-749-873-132	Sequence 132, Appli
6	523	79.8	136	11	US-09-749-873-99	Sequence 99, Appli
7	523	79.8	269	11	US-09-749-873-109	Sequence 109, Appli
8	492	75.1	117	10	US-09-158-120A-17	Sequence 17, Appli
9	492	75.1	119	15	US-10-233-996-41	Sequence 11, Appli
10	491.5	75.0	245	11	US-09-880-748-896	Sequence 1896, Appli
11	486	74.2	140	15	US-10-283-349-63	Sequence 63, Appli
12	486	74.2	143	12	US-10-428-662-69	Sequence 69, Appli
13	485.5	74.1	120	14	US-10-025-687-2	Sequence 2, Appli
14	485.5	74.1	120	15	US-10-125-687-2	Sequence 2, Appli
15	484	73.9	180	9	US-09-748-960-6	Sequence 6, Appli

RESULT 1
US-10-056-794-19
; Sequence 19, Application US/10056794
; Publication No. US20030119078A1
; GENERAL INFORMATION:
; APPLICANT: Graves, Scott S.
; Reno, John M.
; Hyaridis, Robert W.
; Hyaridis, Mark D.
; Searle, Stephen M.J.
; Henry, Andrew H.
; Pedersen, Jan T.
; Rees, Anthony R.

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN PRETARGETTING METHODS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA

ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2002
APPLICATION NUMBER: US/10/056,794
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey Ph.D., Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE DOCKET NUMBER: 690022.527C2
TELECOMMUNICATION INFORMATION:

RESULT 3
 US-10-013-173-4
 / Sequence 4, Application US/10013173
 / Publication No. US200301095377A1
 / GENERAL INFORMATION:
 / APPLICANT: Goshorn, Stephen C.
 / APPLICANT: Graves, Scott Stoll
 / APPLICANT: Schultz, Joanne Elaine
 / APPLICANT: Lin, Yukang
 / APPLICANT: Sanderson, James A.
 / APPLICANT: Reno, John M.
 / TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 / METHODS OF USE THEREOF
 / FILE REFERENCE: 690022.547C1
 / CURRENT APPLICATION NUMBER: US/10/013,173
 / CURRENT FILING DATE: 2001-12-07
 / NUMBER OF SEQ ID NOS: 69
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 4
 / LENGTH: 431
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Predicted amino acid sequence for hnr-LU-10
 / OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
 US-10-013-173-4

Query Match 79.9%; Score 523.5; DB 15; Length 120;
 Best Local Similarity 82.9%; Pred. No. 4.6e-43; Indels 3; Gaps 1;
 Matches 102; Conservative 8; Mismatches 10;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGPNIKOTYIHWVROAQQRLEWMGRIDPANGTKY 60
 Db 1 QVQLVQSGAEVKPGASVKVSKASGPNIKOTYIHWVROAQQRLEWMGRIDPANGTKC 60

Qy 61 DPFKQGRVTITADTSASTAYMELSSRLSDTAVYCSREVL--TGTWSLDYWGQSTLV 120
 Db 61 DLSFQGRVTITADTSINTAYMELSSRLSDTAVYCSREVL--TGTWSLDYWGQSTLV 117

Qy 121 VSS 123
 Db 118 VSS 120

RESULT 2
 US-10-244-821-4
 / Sequence 4, Application US/10244821
 / Publication No. US20030143233A1
 / GENERAL INFORMATION:
 / APPLICANT: Goshorn, Stephen Charles
 / APPLICANT: Graves, Scott Stoll
 / APPLICANT: Schultz, Joanne Elaine
 / APPLICANT: Lin, Yukang
 / APPLICANT: Sanderson, James Allen
 / APPLICANT: Reno, John M.
 / APPLICANT: Dearstyne, Erica A.
 / TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 / METHODS OF USE THEREOF
 / FILE REFERENCE: 690022.547C3
 / CURRENT APPLICATION NUMBER: US/10/244,821
 / CURRENT FILING DATE: 2002-09-16
 / NUMBER OF SEQ ID NOS: 92
 / SEQ ID NO 4
 / LENGTH: 431
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Predicted amino acid sequence for hnr-LU-10
 / OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
 US-10-244-821-4

Query Match 79.9%; Score 523.5; DB 12; Length 431;
 Best Local Similarity 82.9%; Pred. No. 1.9e-42; Indels 3; Gaps 1;
 Matches 102; Conservative 8; Mismatches 10;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGPNIKOTYIHWVROAQQRLEWMGRIDPANGTKY 60
 Db 148 QVQLVQSGAEVKPGASVKVSKASGPNIKOTYIHWVROAQQRLEWMGRIDPANGTKS 207

Qy 61 DPFKQGRVTITADTSASTAYMELSSRLSDTAVYCSREVL--TGTWSLDYWGQSTLV 120
 Db 208 DLSFQGRVTITADTSINTAYMELSSRLSDTAVYCSREVL--TGTWSLDYWGQSTLV 264

Qy 121 VSS 123
 Db 265 VSS 267

RESULT 4
 US-10-150-762-4
 / Sequence 4, Application US/10150762
 / Publication No. US20030103946A1
 / GENERAL INFORMATION:
 / APPLICANT: Goshorn, Stephen C.
 / APPLICANT: Graves, Scott S.
 / APPLICANT: Schultz, Joanne E.
 / APPLICANT: Sanderson, James A.
 / APPLICANT: Reno, John M.
 / APPLICANT: Dearstyne, Erica A.
 / TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 / METHODS OF USE THEREOF
 / FILE REFERENCE: 690022.547C2
 / CURRENT APPLICATION NUMBER: US/10/150,762
 / CURRENT FILING DATE: 2002-05-17
 / NUMBER OF SEQ ID NOS: 90
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO 4
 / LENGTH: 431
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Predicted amino acid sequence for hnr-LU-10
 / OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
 US-10-150-762-4

Query Match 79.9%; Score 523.5; DB 15; Length 431;

RESULT 3		RESULT 4	
HV07 MOUSE		HV1B HUMAN	
AC	HV07 MOUSE	STANDARD;	PRT;
DT	P01751; P01752;		139 AA.
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	21-JUL-1986 (Rel. 01, Last annotation update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DR	1 QVQLYSGAEVKPGKPSVKSCKASGFNIKDTYIHWVQAPGQLEWNGRIDPANGTYK 60		15-SEP-2003 (Rel. 42, Last annotation update)
DR	20 QVQLYSGAEVKPGKPSVKSCKASGFNIKDTYIHWVQAPGQLEWNGRIDPANGTYK 79		Ig heavy chain V region B1-8/186-2 precursor.
DR	61 DPKFQGRVYTADTSASTAYMELSLRSRDTAVYCAR----EGYXGNYGVYAMDYQGTYQ 115		Mus musculus (Mouse).
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		NCBI_TaxID=10090;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		[1]
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		SEQUENCE FROM N.A.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		STRAIN=C57BL/6;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		MEDLINE=123448; PubMed=6788376;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Cell 24:625-637(1981).
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		-!- MISCELLANOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTR (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announe/ or send an email to license@isb-sib.ch).
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		[1]
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		SEQUENCE FROM N.A.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		MEDLINE=81131846; PubMed=186198;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Marshak-Rothstein A.;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		"The genetic basis of antibody production: the dominant anti-arsenite idiotype response of the strain A mouse.";
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		RL. J. Immunol. 12:1023-1032(1982).
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		-!- MISCELLANOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		DR HSSP; P01759; IMCP.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		InterPro; IPR007110; Ig-like.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		InterPro; IPR03006; Ig_MHC.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		InterPro; IPR003596; Ig_v.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		InterPro; IPR004047; Ig; 1.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		SMART; SM00405; IgV; 1.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PROSITE; PS50835; Ig_LIKE; 1.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		KW Immunoglobulin V region; Signal; 3D-structure.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT SIGNAL
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		1 19
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		IG HEAVY CHAIN V REGION B1-8/186-2.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT CHAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		20 139
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		FRAMWORK-1.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT DOMAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		50 54
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		COMPLEMENTARITY-DETERMINING-1.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT DOMAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		55 68
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		COMPLEMENTARITY-DETERMINING-2.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT DOMAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		69 85
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		COMPLEMENTARITY-DETERMINING-3.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT DOMAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		86 117
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		D SEGMENT
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT DOMAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		118 124
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		JH2 SEGMENT.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT DOMAIN
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		125 139
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		BY SIMILARITY.
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		PT NON-TER
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		139 139
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		SEQUENCE 139 AA; 15419 MW; 1B57DD4D0C9F465 CRC64;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Query Match 62.4%; Score 4085; DB 1; Length 139;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Best Local Similarity 62.6%; Pred. No. 8.6e-35; Mismatches 18; Indels 3; Gaps 1;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Matches 77; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Qy 1
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		1 QVQLYSGAEVKPGKPSVKSCKASGFNIKDTYIHWVQAPGQLEWNGRIDPANGTYK 61
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Db 1 VQQLYSGAEVKPGKPSVKSCKASGFNIKDTYIHWVQAPGQLEWNGRIDPANGTYK 60
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Qy 62 PKTQGRVYTADTSASTAYMELSLRSRDTAVYCAR----EGYXGNYGVYAMDYQGTYQ 121
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Db 61 EKPKGKPTLTVDRQSLTSSTAYMQLRSLTSSTAYFCARSVYQGTYQ 118
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Qy 122 SS 123
DR	80 APRFQGRVMTDRASFSTAYMELSLRSRDTAVYCAR----GTYFDTWQGQTLTV 118		Db 119 SS 120

Sequence 24, Application US/07791213D
 GENERAL INFORMATION:
 APPLICANT: MORISHITA, Hideaki
 APPLICANT: KANAMORI, Toshinori
 APPLICANT: NOBUTARA, Masahiro
 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE SAME, AND ENZYME
 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND METHODS OF
 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/791,213D
 FILING DATE: 13-NOV-1991
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 2-306745
 FILING DATE: 13-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M
 REGISTRATION NUMBER: 36,607
 REFERENCE/DOCKET NUMBER: 029650-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-791-213D-40

Query Match Similarity 0.0%; Score 0; DB 1; Length 1;
 Best Local Similarity 0.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 X 1
 Db 1 C 1

RESULT 4
 US-08-174-365A-57
 Sequence 57, Application US/08174365A
 GENERAL INFORMATION:
 Patent No. 5478809
 APPLICANT: Seiichi TANIDA et al.
 TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack
 STREET: 805 Fifteenth Street, N.W., #700
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/174,365A
 FILING DATE: December 28, 1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 INFORMATION FOR SEQ ID NO: 57:

Sequence 24, Application US/07791213D
 GENERAL INFORMATION:
 APPLICANT: MORISHITA, Hideaki
 APPLICANT: KANAMORI, Toshinori
 APPLICANT: NOBUTARA, Masahiro
 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE SAME, AND ENZYME
 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND METHODS OF
 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States

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DM protein - protein search, using sw model

Run on: November 21, 2003, 15:21:14 ; Search time 2.77397 Seconds
(without alignments)
520.023 Million Cell updates/sec

Title: US-09-010-377-3
Perfect score: 15
Sequence: 1 XXXXXXXXXXXXXXXX 15

Scoring table: BL2SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : PIR 76.4*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	0	0.0	3	3	RHTDDO		thyroloberin - Bom
2	0	0.0	3	3	RHPTG		thyroloberin - pig
3	0	0.0	3	3	RHSHT		thyroloberin - she
4	0	0.0	3	3	A92971		thyroloberin - eas
5	0	0.0	3	3	GKHU		growth-modulating
6	0	0.0	3	3	A60898		bursin - chicken
7	0	0.0	3	3	A23751		spinal cord peptid
8	0	0.0	3	3	B23751		thyrolobulin - release
9	0	0.0	3	3	A33802		R-phycocerythrin al
10	0	0.0	3	3	A22565		angiotensin-conver
11	0	0.0	3	3	PQ0010		histidino dehydro
12	0	0.0	3	3	S13894		TRH-like tripeptid
13	0	0.0	3	3	A43391		bradykinin potent
14	0	0.0	3	3	E37196		gene p20K protein
15	0	0.0	3	3	F37196		T-cell receptor be
16	0	0.0	3	3	I50412		T-cell receptor be
17	0	0.0	3	3	PT0636		T-cell receptor be
18	0	0.0	3	3	PT0578		T-cell receptor be
19	0	0.0	3	3	PT0571		T-cell receptor be
20	0	0.0	3	3	PT0622		tyrosine protein k
21	0	0.0	3	3	178890		blood cell protein
22	0	0.0	3	3	SE8328		cytochrome-c oxida
23	0	0.0	3	3	TI3892		antho-RFamide neu
24	0	0.0	4	1	ECXAA		thyroglobulin - do
25	0	0.0	4	2	S18401		phagocytosis stimu
26	0	0.0	4	2	A92147		tyrosine melanocyt
27	0	0.0	4	2	A32039		cardioexcitatory n
28	0	0.0	4	2	ECNK		carbon-monoxide de
29	0	0.0	4	2	PLO140		

ALIGNMENTS

RESULT 1	RHTDDO	thyroloberin - Bombina orientalis	C;Species: Bombina orientalis	C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
			C;Accession: A90919; A0145	R;Yasuhara, T.; Nakajima, T.; Chem. Pharm. Bull. 23, 301-3303, 1975
			A;Title: Occurrence of Pyr-His-Pro-NH ₂ in the frog skin.	A;Reference number: A9019; MUID:76138399; PMID:815011
			A;Molecule type: protein	A;Accession: A90919
			A;Residues: 1-3 <PAS>	A;Superfamily: thyroloberin precursor
			C;Keywords: amidated carboxylic acid end (Gln) #status experimental	C;Keywords: amidated carboxylic acid (Gln) #status experimental
			F;1;Modified site: amidated carboxyl end (Pro) #status experimental	F;3;Modified site: amidated carboxyl end (Pro) #status experimental
			Query Match 0.0% ; Score 0 ; DB 3 ; Length 3 ;	Query Match 0.0% ; Score 0 ; DB 3 ; Length 3 ;
			Best Local Similarity 0.0% ; Pred. No. 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;	Best Local Similarity 0.0% ; Pred. No. 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
RESULT 2	RHPTG	thyroloberin - pig	C;Species: Sus scrofa domestica (domestic pig)	C;Species: Sus scrofa domestica (domestic pig)
			C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001	C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
			C;Accession: A0145	R;Boeler, J.; Brämann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
			C;Contents: annotation	R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.
			A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing hormone	A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing hormone
			A;Reference number: A90167; MUID:7039904; PMID:4982117	A;Reference number: A90167; MUID:7039904; PMID:4982117
			Biochem. Biophys. Res. Commun. 37, 705-710, 1969	Biochem. Biophys. Res. Commun. 37, 705-710, 1969
			A;Contents: biological activities and Rf values (in 17 chromatographic systems) of the synthe	A;Contents: biological activities and Rf values (in 17 chromatographic systems) of the synthe
			C;Superfamily: thyroloberin precursor	C;Superfamily: thyroloberin precursor
			C;Keywords: amidated carboxylic acid end (Gln) #status experimental	C;Keywords: amidated carboxylic acid end (Gln) #status experimental
			F;1;Modified site: amidated carboxyl end (Pro) #status experimental	F;1;Modified site: amidated carboxyl end (Pro) #status experimental
			Query Match 0.0% ; Score 0 ; DB 3 ; Length 3 ;	Query Match 0.0% ; Score 0 ; DB 3 ; Length 3 ;

Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Matches 0; Conservative 0;

QY 1 X 1

Db 1 Q 1

RESULT 3

RHSHT thyroloberin - sheep

C;Species: Ovis orientalis aries. Ovis ammon aries (domestic sheep)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A01421

R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.

Experientia 33, 324-325; 1977

A;Title: Growth-modulating serum tripeptide is glycyl histidyl-lysine.

A;Reference number: A01421; MUID:77162369; PMID:858356

A;Accession: A01421

A;Molecule type: protein

A;Residues: 1-3 <SCH>

A;Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit unassigned animal peptides

C;Species: Gallus gallus (chicken)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A60898

R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.

Science 231, 997-999; 1986

A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the chicken

A;Reference number: A60898; MUID:86122916; PMID:3484838

A;Accession: A60898

A;Molecule type: Protein

A;Residues: 1-3 <AUD>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hormone

F;3/Modified site: amidated carboxyl end (Gly) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Matches 0; Conservative 0;

QY 1 X 1

Db 1 Q 1

RESULT 4

A92971 thyroloberin - eastern newt (tentative sequence)

C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A92971; A01415

R;Grimm-Jorgensen, Y.; McKey, J.F.

J. Neurochem. 23, 471-478; 1974

A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain

A;Reference number: A92971; MUID:4219528

A;Accession: A92971

A;Molecule type: protein

A;Residues: 1-3 <SRI>

A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrotropin, or glutamic acid

C;Superfamily: thyroloberin precursor

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic acid

F;3/Modified site: pyroglutamine carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Matches 0; Conservative 0;

QY 1 X 1

Db 1 Q 1

RESULT 5

GHU growth-modulating peptide - human

GenCore version 5.1.6
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protein - protein search, using sw model

on: November 21, 2003, 15:20:03 ; Search time 1.48973 Seconds
 (without alignments)
 473.510 Million cell updates/sec

Title: US-09-010-377-3
 Effect score: 15
 Sequence: 1 XXXXXXXXXXXX 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
 Overall number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	0	0.0	3	1	GRWM_HUMAN	P01157 homo sapiens
2	0	0.0	3	1	LUXE_VIBRIFI	P24272 vibrio fife
3	0	0.0	3	1	THYL_PIG	P01151 suis scrofa
4	0	0.0	4	1	ACH1_ACHEU	P35904 achatina fulica
5	0	0.0	4	1	DML_PSECH	P19116 pseudomonas
6	0	0.0	4	1	DOMS_PSECH	P19118 pseudomonas
7	0	0.0	4	1	BOSI_HUMAN	P02731 homo sapiens
8	0	0.0	4	1	PAR3_HIRME	P42562 hirudo medicinalis
9	0	0.0	4	1	PAR4_HIRME	P42563 hirudo medicinalis
10	0	0.0	4	1	FFKA_ANTEL	P48705 anthopelus
11	0	0.0	4	1	FLRF_HIRME	P42561 hirudo medicinalis
12	0	0.0	4	1	FLRN_ANTEL	P58707 anthopelus
13	0	0.0	4	1	FMRF_MACNI	P01162 macrocallia
14	0	0.0	4	1	FYRI_ANTEL	P58708 anthopelus
15	0	0.0	4	1	OCP1_OCTMI	P58548 octopus macropus
16	0	0.0	4	1	OCP3_OCTMI	P58649 octopus macropus
17	0	0.0	4	1	RM01_BEAST	P36515 saccharomyces
18	0	0.0	4	1	TUFT_HUMAN	P01858 homo sapiens
19	0	0.0	5	1	AL14_CARMA	P81817 carcinus maenas
20	0	0.0	5	1	BIOA_CITFR	P13071 citrobacter freundii
21	0	0.0	5	1	BIOB_CITFR	P12397 citrobacter freundii
22	0	0.0	5	1	BPP7_BOTIN	P30425 bothrops
23	0	0.0	5	1	B103_LITRU	P82019 litoria rubra
24	0	0.0	5	1	B104_LITRU	P82100 litoria rubra
25	0	0.0	5	1	FARP_ARTTR	P41853 artiposthia
26	0	0.0	5	1	PAP2_BARMA	P41864 pardachirus
27	0	0.0	5	1	PRCT_PERAM	P01373 periplaneta americana
28	0	0.0	5	1	PSK_DAUCA	P58861 daucus carota
29	0	0.0	5	1	REB1_LITRU	P82070 litoria rubra
30	0	0.0	5	1	RE21_LITRU	P82071 litoria rubra
31	0	0.0	5	1	RE31_LITRU	P82072 litoria rubra
32	0	0.0	5	1	SUGA_ACHINDO	P82013 litoria rubra
33	0	0.0	5	1	SUGA_ACHINDO	P19991 achaea domesticus

CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC

EMBL: M62812 ; NOT_ANNOTATED_CDSS.
 DR Luminescence; Ligase.
 KW PIR; A90159; RHTD10.
 SF PIR; A92971; A92971.
 SQ PIR; A9350; RHSHT.
 SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;
 SEQUENCE 1 AA; 1 PYRROLIDONE CARBOXYLIC ACID.
 SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 X 1
 Db 1 I 1

RESULT 3
 THYL_PIG STANDARD; PRT; 3 AA.
 ID THYL_PIG
 AC P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thyrolyberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
 OS Sus scrofa (Pig).
 OS Ovis aries (Sheep).
 OS Bombina orientalis (Oriental fire-bellied toad), and
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens);
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Metazoa; Eutheria; Cetartiodactyla; Suinae; Suidae; Sus.
 OX NCBI_TAXID:9823, 9940, 8346, 8316;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Pig; TISSUE=Hypothalamus;
 RX MEDLINE=70039904; PubMed=4982117;
 RA Boeler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 RT releasing hormone and pyroglutamyl-histidyl-proline amide.";
 RT Biochem. Biophys. Res. Commun. 37:705-710(1969).
 RL [2]
 RN SYNTHESIS.
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Hypothalamus;
 RX MEDLINE=1013386; PubMed=4985794;
 RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemain R.,
 RA Ward D.N.;
 RA "The elucidation of the primary structure of the hypothalamic thyroid
 RT stimulating hormone releasing factor of ovine origin by means of mass
 RT spectrometry.";
 RL Org. Mass Spectrom. 5:221-228(1971).
 RN SYNTHESIS.
 RP SPECIES=Sheep;
 RC TISSUE=Heart atrium;
 RX MEDLINE=91264986; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Matsumoto Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RA "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=ferussac; TISSUE=Heart atrium;
 RX MEDLINE=89273551; PubMed=259281;
 RA Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 177:847-853 (1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,

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QTM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:39 ; Search time 6.4726 Seconds

(without alignments)
598.027 Million cell updates/sec

Title: US-09-010-377-3

Jefreffect score: 15

Sequence: 1 XXXXXXXXXXXXXXXX 15

Scoring table: BL003M62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23.1*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_invertebrate:*

5: sp_mammal:*

6: sp_mhc:*

7: sp_phage:*

8: sp_organelle:*

9: sp_rhagie:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteria:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	%
1	0	0.0	4	11	Q08433	Q08433 ratmus sp.	
2	0	0.0	5	2	P83073	P83073 bacillus ce	
3	0	0.0	5	10	Q99907	Q99907 hordeum vul	
4	0	0.0	5	13	P83308	P83308 gallus gall	
5	0	0.0	6	10	P82281	P82281 spinacia ol	
6	0	0.0	6	10	P82241	P82241 spinacia ol	
7	0	0.0	6	10	P82282	P82282 spinacia ol	
8	0	0.0	7	2	Q8KMS3	Q8KMS3 klebsiella	
9	0	0.0	7	2	Q47505	Q47505 escherichia	
10	0	0.0	7	2	P70804	P70804 azotobacter	
11	0	0.0	7	2	050556	050556 actinobacil	
12	0	0.0	7	2	Q47477	Q47477 escherichia	
13	0	0.0	7	2	Q47029	Q47029 enterobacte	
14	0	0.0	7	2	P72081	P72081 nocardia la	
15	0	0.0	7	2	Q54248	Q54248 streptomyce	
16	0	0.0	7	2	Q8KMS9	Q8KMS9 enterobacte	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCE FROM N A.

RC STRAIN-Gunn;

RX MEDLINE=91232758; PubMed=1840486;

RA Sato H, Aono S, Kashiwabara S, Koiwai O;

RT genetic defect of bilirubin UDP-glucuronosyltransferase (Fragment).

DE Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Rattus.

OX NCBI-TaxID=10118;

RN [1]

RP STRAIN-Gunn;

RC MEDLINE=91232758; PubMed=1840486;

RA Sato H, Aono S, Kashiwabara S, Koiwai O;

RT genetic defect of bilirubin UDP-glucuronosyltransferase (Fragment).

DE Rattus sp.

OC hyperbilirubinemic Gunn rat.;"

RL Biochem Biophys Res Commun. 177:1161-1164(1991).

DR EMBL; S38636; AAB19259.1; -.

DR NCBI-TaxID=10118;

RN

SEQUENCE FROM N A.

RC STRAIN-Gunn;

RX MEDLINE=91232758; PubMed=1840486;

RA Sato H, Aono S, Kashiwabara S, Koiwai O;

RT genetic defect of bilirubin UDP-glucuronosyltransferase in the

RT hyperbilirubinemic Gunn rat.;"

RL Biochem Biophys Res Commun. 177:1161-1164(1991).

DR Transferase.

KW NON TER

FT SEQUENCE

SQ 1 4 AA; 473 MW; 633732C42000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DR 1 N 1

ID P83073

AC P83073;

DT 01-OCT-2001 (TREMBLrel. 18, Created)

RESULT 1

Q08433 PRELIMINARY;

ID Q08433; PRT;

AC 0. AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Bilirubin UDP-glucuronosyltransferase (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Rattus.

OX NCBI-TaxID=10118;

RN [1]

RP STRAIN-Gunn;

RC MEDLINE=91232758; PubMed=1840486;

RA Sato H, Aono S, Kashiwabara S, Koiwai O;

RT genetic defect of bilirubin UDP-glucuronosyltransferase in the

RT hyperbilirubinemic Gunn rat.;"

RL Biochem Biophys Res Commun. 177:1161-1164(1991).

DR Transferase.

KW NON TER

FT SEQUENCE

SQ 1 4 AA; 473 MW; 633732C42000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1

DR 1 N 1

ID P83073

AC P83073;

DT 01-OCT-2001 (TREMBLrel. 18, Created)

RESULT 2

Q8KMS3 PRELIMINARY;

ID P83073

AC P83073;

DT 01-OCT-2001 (TREMBLrel. 18, Created)

RESULT 3
 ID P899007 PRELIMINARY; PRT; 5 AA.
 AC Q99007; 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 AC 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 AC 88 kDa Protein (Fragment).
 AC Bacillus cereus.
 AC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 AC NCBI_TaxID=1396;
 AC [1]
 SEQUENCE
 STRAIN=NCTMB 11796;
 RA Brown N., Dowds B.C.A.;
 RA Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5 5 MW; 6B01AAA336F00000 CRC64;
 SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
 Query Match Score 0; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 X 1
 Db 4 T 4

RESULT 4
 ID P833308 PRELIMINARY; PRT; 5 AA.
 AC P833308; 01-OCT-2001 (TREMBLrel. 21, Created)
 AC 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 AC 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 AC FMRFamide-like neuropeptide (LPRRF-amide).
 AC Galus galus (Chicken).
 AC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Archosauvia Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 AC NCBI_TaxID=9031;
 SEQUENCE, AND SYNTHESIS.
 RP

RESULT 5
 ID P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181; 01-JUN-2000 (TREMBLrel. 14, Created)
 AC 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 AC 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 AC Chloroplast 50S ribosomal protein L10 beta (Fragment).
 AC Spinacia olaracea (Spinach).
 AC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 AC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 AC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 AC NCBI_TaxID=3586;
 RN [1]
 SEQUENCE ALWARO; TISSUE=Leaf;
 RC STRAIN=CV7; PubMed=10574046;
 RX MEDLINE=0435798; PubMed=10574046;
 RA Yamaguchi K.; Subramanian A. R.;
 RA "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482 (2000).
 AC FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -|- SIMILARITY: BELONGS TO THE L10 FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal L10.
 DR InterPro: IPR002363; Ribosomal L10eub.
 DR Pfam: PF0466; Ribosomal L10, PARTIAL.
 DR PROSITE: PS01109; Ribosomal L10, PARTIAL.
 DR Ribosomal Protein; Chloroplast; rRNA-binding.
 FT NON_TER 6 6 MW; 6321B415B05DB000 CRC64;
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

RESULT 6
 ID P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541; 01-OCT-2000 (TREMBLrel. 15, Created)
 AC 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 AC 01-JUN-2001 (TREMBLrel. 17, Last annotation update).
 AC Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia olaracea (Spinach).
 OS

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M protein - protein search, using sw model

un on: November 21, 2003, 15:19:18 ; Search time 16.6438 Seconds
 (without alignments)
 285.100 Million cell updates/sec

title: perfect score: US-09-010-377-4

sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXX 30

coring table: BL05062 Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database: A_Genesed_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

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12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

1 AAY46652 standard; Peptide; 1 AA.

1 ID AAY46652 (first entry)

1 DT 01-DEC-1999

1 XX Immunogenic peptide having a human leukocyte antigen binding motif #1263.

1 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.

1 XX Synthetic.

1 OS Homo sapiens.

1 XX WO9945954-A1.

1 PD 16-SEP-1999.

1 XX 13-MAR-1998; 9BWO-US05039.

1 XX 13-MAR-1998; 9BWO-US05039.

1 XX (EPIM-) EPIMMUNE INC.

1 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

1 XX DR WPI: 1999-551214/46.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	0	0.0	1	20	AAY46652		Immunogenic peptide
2	0	0.0	1	22	ABBG6870		Human SNP related
3	0	0.0	1	22	ABBG6809		Drosophila melanog
4	0	0.0	1	22	ABBG6810		Novel human diagno
5	0	0.0	1	22	ABG2941		Human Peptide #918
6	0	0.0	1	22	AAM97643		Human Peptide #110
7	0	0.0	1	22	AAM7834		Human Peptide #124
8	0	0.0	1	22	AAM97974		Human Peptide #162
9	0	0.0	1	22	AAM98354		

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OM protein - protein search, using sw model

Run on: November 21, 2003, 15:21:54 ; Search time 5.65068 seconds
(without alignments)
224.652 Million cell updates/sec

Perfect score: US-09-010-377-4

Sequence: 30 XXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:
1: /cgm2_6/prodata/1/1iaa/5A_COMB_pep:
2: /cgm2_6/prodata/1/1iaa/5B_COMB_pep:
3: /cgm2_6/prodata/1/1iaa/6A_COMB_pep:
4: /cgm2_6/prodata/1/1iaa/6B_COMB_pep:
5: /cgm2_6/prodata/1/1iaa/pcrtr COMB_pep:
6: /cgm2_6/prodata/1/1iaa/backfilles1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	0	0.0	1	1	US-07-820-154A-12	Sequence 12, App1	
2	0	0.0	1	1	US-07-791-213D-24	Sequence 24, App1	
3	0	0.0	1	1	US-07-791-213D-40	Sequence 10, App1	
4	0	0.0	1	1	US-08-174-165A-57	Sequence 57, App1	
5	0	0.0	1	1	US-07-789-913-23	Sequence 23, App1	
6	0	0.0	1	1	US-07-789-913-25	Sequence 25, App1	
7	0	0.0	1	1	US-08-049-94-23	Sequence 23, App1	
8	0	0.0	1	1	US-08-049-794-25	Sequence 25, App1	
9	0	0.0	1	1	US-08-433-037-12	Sequence 12, App1	
10	0	0.0	1	1	US-08-448-606-4	Sequence 4, App1	
11	0	0.0	1	1	US-07-869-933-16	Sequence 16, App1	
12	0	0.0	1	1	US-08-293-150A-24	Sequence 24, App1	
13	0	0.0	1	1	US-08-293-150A-40	Sequence 40, App1	
14	0	0.0	1	1	US-08-296-847-25	Sequence 23, App1	
15	0	0.0	1	1	US-08-49-847-25	Sequence 25, App1	
16	0	0.0	1	2	US-08-742-774-23	Sequence 23, App1	
17	0	0.0	1	2	US-08-742-774-25	Sequence 25, App1	
18	0	0.0	1	2	US-08-675-354-23	Sequence 23, App1	
19	0	0.0	1	2	US-08-675-354-25	Sequence 25, App1	
20	0	0.0	1	2	US-08-097-554A-12	Sequence 12, App1	
21	0	0.0	1	2	US-08-965-918-25	Sequence 23, App1	
22	0	0.0	1	2	US-08-965-918-25	Sequence 25, App1	
23	0	0.0	1	2	US-09-138-439-23	Sequence 23, App1	
24	0	0.0	1	2	US-09-138-439-25	Sequence 25, App1	
25	0	0.0	1	3	US-08-680-640A-12	Sequence 12, App1	
26	0	0.0	1	3	US-08-613-400A-23	Sequence 23, App1	
27	0	0.0	1	3	US-08-613-400A-25	Sequence 25, App1	

RESULT 2
US-07-791-213D-24

RESULT 1
US-07-820-154A-12

ALIGNMENTS

28	0	0.0	1	3	US-08-801-092-10	Sequence 10, App1
29	0	0.0	1	3	US-08-801-092-17	Sequence 17, App1
30	0	0.0	1	3	US-08-801-092-24	Sequence 24, App1
31	0	0.0	1	3	US-08-801-092-31	Sequence 31, App1
32	0	0.0	1	3	US-08-801-092-38	Sequence 38, App1
33	0	0.0	1	3	US-08-801-092-45	Sequence 45, App1
34	0	0.0	1	3	US-09-298-017-23	Sequence 23, App1
35	0	0.0	1	3	US-08-295-802-12	Sequence 12, App1
36	0	0.0	1	3	US-09-392-979A-23	Sequence 23, App1
37	0	0.0	1	3	US-09-392-979A-25	Sequence 25, App1
38	0	0.0	1	3	US-09-103-663-16	Sequence 16, App1
39	0	0.0	1	3	US-08-488-37A-12	Sequence 12, App1
40	0	0.0	1	3	US-09-117-927-5	Sequence 5, App1
41	0	0.0	1	4	US-08-375-992A-12	Sequence 12, App1
42	0	0.0	1	4	US-09-315-113-10	Sequence 10, App1
43	0	0.0	1	4	US-09-315-113-17	Sequence 17, App1
44	0	0.0	1	4	US-09-315-113-24	Sequence 24, App1

Sequence 24, Application US/07791213D
 Patent No. 5409895
 GENERAL INFORMATION:
 APPLICANT: MORISHITA, Hideaki
 APPLICANT: KANAMORI, Toshinori
 APPLICANT: NOBUHARA, Masahiro
 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE SAME, AND ENZYME
 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 TITLE OF INVENTION: TREATING USING THE SAME
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/791,213D
 FILING DATE: 13-NOV-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 2-306745
 FILING DATE: 13-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Meuth, Donna M.
 REGISTRATION NUMBER: 35,607
 REFERENCE/DOCKET NUMBER: 029650-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 S-07-791-213D-24

Query	Match	0.0%	Score	0;	DB	1;	Length	1;
Best	Local	Similarity	0.0%;	Pred	No.	0;	Indels	0;
Matches	0;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps
Y		1 X 1						
Y		1 C 1						
b								

RESULT 3
 S-07-791-213D-40
 Sequence 40, Application US/07791213D
 Patent No. 5409895
 GENERAL INFORMATION:
 APPLICANT: MORISHITA, Hideaki
 APPLICANT: KANAMORI, Toshinori
 APPLICANT: NOBUHARA, Masahiro
 TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE SAME, AND ENZYME
 TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 TITLE OF INVENTION: TREATING USING THE SAME
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States

```

ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mouth, Donna M
REGISTRATION NUMBER: 35,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-40

Query Match Score 0; DB 1; Length 1
Best Local Similarity 0.0%; Pred. NO. 0;
Matches 0; Conservative 0; Mismatches 1;
I
Qy 1 X 1
Db 1 C 1

RESULT 4
US 08-174-365A-57
; Sequence 57, Application US/08174365A
; Patent No. 5418809
GENERAL INFORMATION:
APPLICANT: Seiichi TANIDA et al.
TITLE OF INVENTION: 4-(THIAHEPTANOIC ACID DERIVATIVE)
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,365A
FILING DATE: December 28, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
INFORMATION FOR SEQ ID NO: 57:

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 21, 2003, 15:27:54 ; Search time 11.1986 Seconds

(without alignments)
489.058 Million cell updates/sec

Title: US-09-010-377-4

Perfect score: 30

Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62

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Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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16: /cgn2_6_ptodata/1/pubpaa/us10C_PUBCOMB.pep:*

17: /cgn2_6_ptodata/1/pubpaa/us10_NEW_PUB.pep:*

18: /cgn2_6_ptodata/1/pubpaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result % Query Match Length DB ID Description

result No.	Score	Match	Length	DB ID	Description
1	0	0.0	1	9 US-09-909-348-4	Sequence 4, Appli
2	0	0.0	1	10 US-09-982-172-3	Sequence 3, Appli
3	0	0.0	1	10 US-09-982-172-4	Sequence 4, Appli
4	0	0.0	1	10 US-09-982-172-9	Sequence 9, Appli
5	0	0.0	1	10 US-09-982-172-11	Sequence 11, Appli
6	0	0.0	1	10 US-09-982-172-19	Sequence 19, Appli
7	0	0.0	1	10 US-09-982-172-31	Sequence 31, Appli
8	0	0.0	1	10 US-09-982-172-35	Sequence 35, Appli
9	0	0.0	1	10 US-09-982-172-37	Sequence 37, Appli
10	0	0.0	1	10 US-09-982-172-46	Sequence 46, Appli
11	0	0.0	1	10 US-09-982-172-69	Sequence 69, Appli
12	0	0.0	1	10 US-09-982-172-80	Sequence 80, Appli
13	0	0.0	1	10 US-09-982-172-81	Sequence 81, Appli
14	0	0.0	1	10 US-09-982-172-83	Sequence 83, Appli
15	0	0.0	1	10 US-09-982-172-86	Sequence 86, Appli

SEQ ID NO 4 LENGTH: 14

TYPE: PRTR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of Thrombin
NAME/KEY: VARIANT
LOCATION: (1) . . . (14)
OTHER INFORMATION: Xaa at position six is Glu or Gln
OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or
US-09-909-348-4

RESULT 1
US-09-909-348-4

Sequence 4, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; CROWTHOR, Roger S.
; APPLICANT: STIERNBERG, Janet
; APPLICANT: BERGMANN, John
; TITLE OF INVENTION: Stimulation of Cartilage Growth with Agonists
; TITLE OF INVENTION: Stimulation of the No.
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4 LENGTH: 14

Query Match Best Local Similarity 0.0% ; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 V 1

RESULT 2
US-09-982-172-3
; Sequence 3, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3

RESULT 3
US-09-982-172-4
; Sequence 4, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SEQ ID NO: 4
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4

RESULT 4
US-09-982-172-9
; Sequence 9, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283

RESULT 5
US-09-982-172-11
; Sequence 11, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SEQ ID NO: 11
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11

RESULT 6
US-09-982-172-19
; Sequence 19, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SEQ ID NO: 19
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-19

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: November 21, 2003, 15:21:14 ; search time 5.54795 seconds
(without alignments)
520.023 Million cell updates/sec

Title: US-09-010-377-4

Perfect score: 30

Sequence: 1 XXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	Qy	1 X 1	Db	1 Q 1
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2	0	0.0	3	3	RHFTG		thyroloberin - pig				
3	0	0.0	3	3	RHSHT		thyroloberin - she				
4	0	0.0	3	3	A92971		thyroloberin - eel				
5	0	0.0	3	3	GRHU		growth-modulating				
6	0	0.0	3	3	A60898		bursin - chicken				
7	0	0.0	3	3	B23751		spinal cord peptide				
8	0	0.0	3	3	A23751		thyrotropin-releasing				
9	0	0.0	3	3	A33802		hormone				
10	0	0.0	3	3	A22565		R-phycocerythrin				
11	0	0.0	3	3	P00010		angiogenesis-conver				
12	0	0.0	3	3	S13894		histidinol dehydro				
13	0	0.0	3	3	A43391		TRH-like tripeptide				
14	0	0.0	3	3	E37196		bradykinin-potenti				
15	0	0.0	3	3	F37196		gene p200 protein				
16	0	0.0	3	3	I50412		T-cell receptor be				
17	0	0.0	3	3	P0636		T-cell receptor be				
18	0	0.0	3	3	PT0578		T-cell receptor be				
19	0	0.0	3	3	PT0571		tyrosine protein k				
20	0	0.0	3	3	PT0622		blood cell protein				
21	0	0.0	3	3	I78890		cytochrome-c oxida				
22	0	0.0	3	3	S68328		antho-Ranamide neur				
23	0	0.0	3	3	T13892		thyroglobulin - do				
24	0	0.0	4	1	ECXAA		phagocytosis-stimul				
25	0	0.0	4	2	S18401		tyrosine-melanocyt				
26	0	0.0	4	2	A02147		cardioexcitatory n				
27	0	0.0	4	2	A32039		carbon-monoxide de				
28	0	0.0	4	2	ECNK						
29	0	0.0	4	2	PL0140						

Result No.	Score	Query	Match	Length	DB	ID	Description	Qy	1 X 1	Db	1 Q 1
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31	0	0.0	0	0	A37832		phenol 2-monoxyge				
32	0	0.0	0	0	A43360		gamma subunit of P				
33	0	0.0	0	0	I40697		biotin A - Citroba				
34	0	0.0	0	0	A61300		22K superhelical D				
35	0	0.0	0	0	I57745		D-mannose hydro				
36	0	0.0	0	0	A41890		protein D - Escher				
37	0	0.0	0	0	S41014		hypothetical prote				
38	0	0.0	0	0	D41654		cell surface adhes				
39	0	0.0	0	0	B43848		hypothetical prote				
40	0	0.0	0	0	I40505		phospholipase C (B				
41	0	0.0	0	0	I40870		endoglucanase F -				
42	0	0.0	0	0	T46627		hypothetical prote				
43	0	0.0	0	0	S55508		starvation-induced				
44	0	0.0	0	0	S17255		ribosomal protein				

ALIGNMENTS

Result No.	Score	Query	Match	Length	DB	ID	Description	Qy	0.0%	DB 3 ; Length 3 ;	Matches 0 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;
1	0	0.0	0	0	RHTDO		thyrolobelin - Bombina orientalis				
2	0	0.0	0	0	C;Species: Bombina orientalis		C;Sequence_revision 15-Jun-2001 #text_change 15-Jun-2001				
3	0	0.0	0	0	C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001		C;Accession: A90919; A01415				
4	0	0.0	0	0	R;Yasuhara, T.; Nakajima, T.		R;Chem. Pharm. Bull. 23, 3301-3303, 1975				
5	0	0.0	0	0	A;Title: Occurrence of Pyr-His-Pro-NH ₂ in the frog skin.		A;Reference number: A90919; MUID:76138399; PMID:815011				
6	0	0.0	0	0	A;Molecule type: protein		A;Residues: 1-3 <NAs>				
7	0	0.0	0	0	C;Superfamily: thyrolobelin precursor		C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid				
8	0	0.0	0	0	F;1;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental		F;1;Modified site: amidated carboxyl end (Pro) #status experimental				
9	0	0.0	0	0	F;3;Modified site: amidated carboxyl end (Pro) #status experimental		Query Match 0.0% ; Best Local Similarity 0.0% ; Pred. No. 0 ; Mismatches 0 ; Conservati				
10	0	0.0	0	0	0		0.0% ; Score 0 ; DB 3 ; Length 3 ;				
11	0	0.0	0	0	0		Matches 0 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;				
12	0	0.0	0	0	0						
13	0	0.0	0	0	0						
14	0	0.0	0	0	0						
15	0	0.0	0	0	0						
16	0	0.0	0	0	0						
17	0	0.0	0	0	0						
18	0	0.0	0	0	0						
19	0	0.0	0	0	0						
20	0	0.0	0	0	0						
21	0	0.0	0	0	0						
22	0	0.0	0	0	0						
23	0	0.0	0	0	0						
24	0	0.0	0	0	0						
25	0	0.0	0	0	0						
26	0	0.0	0	0	0						
27	0	0.0	0	0	0						
28	0	0.0	0	0	0						
29	0	0.0	0	0	0						

Result No.	Score	Query	Match	Length	DB	ID	Description	Qy	0.0%	DB 3 ; Length 3 ;	Matches 0 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;
1	0	0.0	0	0	RHTDO		thyrolobelin - Bom				
2	0	0.0	0	0	RHFTG		thyrolobelin - pig				
3	0	0.0	0	0	A92971		C;Species: Sus scrofa domestica (domestic pig)				
4	0	0.0	0	0	GRHU		C;Sequence_revision 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001				
5	0	0.0	0	0	A60898		C;Accession: A01415				
6	0	0.0	0	0	B23751		R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.				
7	0	0.0	0	0	A23751		Biochemistry 9, 1103-1106, 1970				
8	0	0.0	0	0	I38890		A;Title: Structure of porcine thyrotropin releasing hormone.				
9	0	0.0	0	0	S68328		A;Reference number: A9067; MUID:70039904; PMID:4982117				
10	0	0.0	0	0	T13892		A;Contents: annotation				
11	0	0.0	0	0	ECXAA		C;Superfamily: thyrolobelin precursor				
12	0	0.0	0	0	S18401		C;Keywords: amidated carboxyl end; hormone; thyroglobulin - do				
13	0	0.0	0	0	A02147		phagocytosis-stimul				
14	0	0.0	0	0	I78890		tyrosine-melanocyt				
15	0	0.0	0	0	S68328		cardioexcitatory n				
16	0	0.0	0	0	T13892		carbon-monoxide de				
17	0	0.0	0	0	ECXAA						
18	0	0.0	0	0	P00571						
19	0	0.0	0	0	PT0578						
20	0	0.0	0	0	PT0622						
21	0	0.0	0	0	I57745						
22	0	0.0	0	0	A22565						
23	0	0.0	0	0	P00010						
24	0	0.0	0	0	S13894						
25	0	0.0	0	0	A43391						
26	0	0.0	0	0	F37196						
27	0	0.0	0	0	I50412						
28	0	0.0	0	0	P0636						
29	0	0.0	0	0	A23751						

Best Local Similarity 0.0%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 0; Qy 1 X 1
 Db 1 Q 1

RESULT 3
 RSHST
 thyroloberin - sheep
 C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
 C;Date: 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A93750; A01415
 R;Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemain, R.; Ward, D.N.
 Org: Mass Spectrom. 5, 221-228, 1971
 A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone
 A;Reference number: A33750
 A;Molecule type: protein
 A;Residues: 1-3 <DESS>
 Nature 226, 321-325, 1970
 A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
 A;Contents: annotation
 A;Note: physicochemical characteristics and biological activities of the natural and synthetic
 C;Keywords: thyroloberin precursor
 C;Modified site: amidated carboxyl end; hormone
 F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 0; Qy 1 X 1
 Db 1 Q 1

RESULT 4
 A92971
 thyroloberin - eastern newt (tentative sequence)
 C;Species: *Notophthalmus viridescens*, *Triturus viridescens* (eastern newt)
 C;Accession: A92971; A01415
 R;Grimm-Jorgensen, Y.; McKelvey, J.F.
 J. Neurochem. 23, 471-478, 1974
 A;Title: Biosynthesis of thyrotropin releasing factor by newt (*Triturus viridescens*) brain
 A;Reference number: A92971; MUID:75035605; PMID:4214528
 A;Accession: A92971
 A;Molecule type: protein
 A;Residues: 1-3 <GRI>
 A;Note: peptide with the chromatographic and electrophoretic characteristics of thyrotropin
 C;Keywords: thyroloberin precursor
 C;Modified site: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic
 F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 X 1
 Db 1 Q 1

RESULT 5
 GKHU
 growth-modulating peptide - human

C;Species: *Homo sapiens* (man)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A01421
 R;Schlesinger, D.H.; Pichart, L.; Thaler, M.M.
 Experientia 33, 324-325, 1977
 A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
 A;Reference number: A01421; MUID:77162369; PMID:858356
 A;Accession: A01421
 A;Molecule type: protein
 A;Residues: 1-3 <SCH>
 A;Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit
 C;Superfamily: unassigned animal peptides

RESULT 6
 A60898
 bursin - chicken
 C;Species: *Gallus gallus* (chicken)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A60898
 R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
 Science 231, 997-999, 1986
 A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the
 A;Reference number: A60898; MUID:86122916; PMID:3484838
 A;Accession: A60898
 A;Molecule type: protein
 A;Residues: 1-3 <AUD>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; hormone
 F;3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 X 1
 Db 1 K 1

RESULT 7
 A23751
 spinal cord peptide SCP-4 - pig
 C;Species: *Sus scrofa domesticus* (domestic pig)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A23751
 R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.-L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
 Arch. Biochem. Biophys. 240, 178-183, 1985
 A;Reference number: A23751; MUID:85250425; PMID:4015098
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-3 <HS1>
 C;Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 X 1
 Db 1 Q 1

RESULT 8

CC	SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.	RT	TSH-releasing factor.;
CC	-!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thioester.	RL	Nature 226:321-325(1970).
CC	-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.	RN	[5]
CC	-----	RP	SEQUENCE; TISSUE=Skin;
CC	-----	RC	SPECIES=B.orientalis;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	MEDLINE=76138399; PubMed=815011;
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	RA	Yasuhara T., Nakajima T.;
CC	the European Bioinformatics Institute. There are no restrictions on its	RT	"Letter: Occurrence of Pro-His-Pro-NH2 in the frog skin.;"
CC	use by non-profit institutions as long as its content is in no way	RL	Chem. Pharm. Bull. 23:3301-3303(1975).
CC	modified and this statement is not removed. Usage by and for commercial	RN	[6]
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	RP	SEQUENCE;
CC	or send an email to license@isb-sib.ch).	RC	SPECIES=N.viridescens;
CC	-----	RC	MEDLINE=5033605; PubMed=4214528;
DR	EMBL: M6:812; -!- NOT_ANNOTATED_CDS.	RC	GRIMM-JORGENSEN Y., McKEELLY J.F.;
KW	Luminescence; Ligase;	RA	"Biogenesis of thyrotropin releasing factor by newt (Triturus
FT	FT	RT	viridescens) brain in vitro. Isolation and characterization of
SEQUENCE	1 MW: 374 MW;	RT	thyrotropin releasing factor.;"
FT	3 AA: 1	RL	J. Neurochem. 23:471-478(1974).
SEQUENCE	6AA: 6AA3303000000000000 CRC64;	CC	-!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
Best Local Similarity 0.0%; Pred. No. 0;	Score 0; DB 1; Length 3;	CC	IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	FT	NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.	
Qy	1 X 1	DR	PIR: A90119; RHTDTC.
Db	1 I 1	DR	PIR: A92271; A922971.
-----	-----	DR	PIR: A93271; A932950; RHTSH.
RESULT 3	THYL_PIG	KW	Amidation; Pyrrolidone carboxylic acid.
ID	THYL_PIG	FT	1 PYRROLIDONE CARBOXYLIC ACID.
AC	P01151;	MOD RES	1
DT	21-JUL-1986 (Rel. 01, Created)	MOD RES	3
DT	21-JUL-1986 (Rel. 01, Last sequence update)	FT	3 AMIDATION.
DT	28-FEB-2003 (Rel. 41, Last annotation update)	SQ	SEQUENCE 3 AA; 380 MW; 7761F6B0000000000 CRCE4;
DB	Thyroliberin, DE	Qy	Query Match 0.0%; Score 0; DB 1; Length 3;
OS	Sus scrofa (Pig);	DB	Best Local Similarity 0.0%; Pred. No. 0;
OS	Ovis aries (Sheep);	Qy	Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OS	Bombina orientalis (Oriental fire-bellied toad), and	DB	-----
OS	Notophthalmus viridescens (Eastern newt) (Triturus viridescens);	-----	-----
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RESULT 4	ACHI_ACHFU STANDARD; PRT;
CC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	AC	P35364; ID=ACHI_ACHFU
OX	NCBI_TAXID=9823, 9940, 8346, 8316;	DT	01-JUN-1994 (Rel. 29, Created)
RP	SEQUENCE.	DT	01-JUN-1994 (Rel. 29, Last sequence update)
RC	SPECIES=PIG; TISSUE=Hypothalamus;	DE	15-JUL-1998 (Rel. 36, Last annotation update)
RC	MEDLINE=70039904; PubMed=198438;	DS	Achatin-1;
RA	Nair R.M.G.; Barrett J.F.; Bowers C.Y.; Schally A.V.;	DS	Achatina fulica (Giant African snail).
RA	"Structure of porcine thyrotropin releasing hormone.;"	OC	Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
RA	Biochem. Biophys. Res. Commun. 37:705-710(1969).	OC	Signoretaria; Achatinoidae; Achatinidae; Achatina.
RA	[2]	NCBI_TAXID=6510; [1]	NCBI_TAXID=6510; [1]
RP	SYNTHESIS.	RN	SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC	SPECIES=PIG;	RP	SEQUENCE, CHARACTERRIZATION; TISSUE=Ganglion;
RC	MEDLINE=70039904; PubMed=1982117;	RC	STRAIN=Perussac;
RA	Boller J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;	RC	STRAIN=Perussac; TISSUE=Heart atrium;
RA	"The identity of chemical and hormonal properties of the thyrotropin	RA	MEDLINE=81264856; PubMed=1675568;
RT	releasing hormone and pyroglutamyl-histidyl-proline amide.;"	RA	Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RT	RA	Yoshida M., Harada A., Munehisa Y., Kobayashi M., Novales-Li P.,	
RL	Org. Mass Spectrom. 5:221-228(1971).	RA	"Purification of achatin-1 from the atria of the African giant snail,"
RN	[4]	RT	Achatina fulica, and its possible function."
RP	SYNTHESIS.	RL	Biochem. Biophys. Res. Commun. 177:847-853(1991).
RC	SPECIES=Sheep; TISSUE=Hypothalamus;	RN	[3]
RC	Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemain R.,	RP	X-RAY CRYSTALLOGRAPHY.
RA	Ward D.N.;	RC	MEDLINE=70163386; PubMed=1985794;
RA	"The elucidation of the primary structure of the hypothalamic thyroid	RA	Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RA	stimulating hormone releasing factor of ovine origin by means of mass	RA	Guillemain R., Inoue M., Inoue Y., Yasuda-Kamatani Y., Minakata H.,
RA	spectrometry.;"	RA	Ishida T., In Y.,
RA	Org. Mass Spectrom. 5:221-228(1971).	RA	"Characterization of ovine hypothalamic hypophysiotropic

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OM protein - protein search, using sw model

run on: November 21, 2003, 15:20:39 ; Search time 12.9452 Seconds

(without alignments)
 596.027 Million cell updates/sec

perfect score: US-09-010-377-4

sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Post-processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodont:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteria:*

17: sp_archeap:*

Preced. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No. Score Query Match Length DB ID Description

1 0.0 0 0 4 11 Q8433 Q8433 rattus sp.

2 0.0 0 0 5 12 P83073 P83073 bacillus ce

3 0.0 0 0 5 10 Q99007 Q99007 hordeum vul

4 0.0 0 0 5 13 P83308 P83308 gallus gall

5 0.0 0 0 6 10 P82281 P82281 spinacia ol

6 0.0 0 0 6 10 P82281 P82281 spinacia ol

7 0.0 0 0 6 10 P82282 P82282 spinacia ol

8 0.0 0 0 7 2 Q8KMS3 Q8KMS3 klebsiella

9 0.0 0 0 7 2 Q47505 Q47505 escherichia

10 0.0 0 0 7 2 P70804 P70804 azotobacter

11 0.0 0 0 7 2 050556 050556 actinobacil

12 0.0 0 0 7 2 Q47477 Q47477 escherichia

13 0.0 0 0 7 2 Q47029 Q47029 enterobacte

14 0.0 0 0 7 2 P72081 P72081 nocardia la

15 0.0 0 0 7 2 Q54248 Q54248 streptomyce

16 0.0 0 0 7 2 Q8KMS9 Q8KMS9 enterobacte

Preced. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCES

SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC SEQUENCE FROM N.A.

034028 sphingomonas

007354 synochococc

089112 borrelia bu

089104 borrelia bu

089100 borrelia bu

015903 homo sapien

Q8nhh7 homo sapien

Q15897 homo sapien

Q28742 oryctolagus

P92214 amblyopyrum

P92393 hordeum vul

P92403 lophopyrum

P92427 peridictyon

Q99182 gnatholepsia

P92430 aegilops ta

P92221 bromus iner

Q98865 spinacia ol

P92425 pseudoroegn

P92381 hordeum bra

P92387 henrardia p

P92210 agropyron c

P92440 thinopyrum

P92218 australopyrum

P92390 heteranthae

P92372 haynaldia v

P92442 taenathera

P92226 crithopsis

Q8mfy6 taraxacum

Q55945 saccharomyces

Q95945

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DT 01-OCT-2001 (TREMBLrel. 18; Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18; Last annotation update)
 88 kDa protein (Fragment).
 OS *Bacillus cereus*.
 NCBI_TaxID=11396;
 [1]
 RN RP

STRAIN=NCIMB 11796;
 RA Browne N.; Dowds B.C.A.;
 RL Submitted (JUN-2001) to the SWISS-PROT data bank.

FT 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
 Db 4 T 4

RESULT 3

Q99007 PRELIMINARY; PRT; 5 AA.

AC 099007; Created)

DT 01-NOV-1996 (TREMBLrel. 01; Created)

DT 01-MAR-2003 (TREMBLrel. 01; Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)

DE Alpha amylase (Fragment).

OS *Hordeum vulgare* (Barley).

Eukaryota; Viridiplantae; Stramenophyta; Embryophyta; Tracheophyta;

SPERMATOPHYTA; Magnoliophyta; euicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

NCBI_TaxID=3562;

RN [1]

SEQUENCE FROM N.A. PubMed=1831055;

RX MEDLINE=91329704; PubMed=1831055;

RA Close T.J.;

RT "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers." Plant Mol. Biol. 16:713-721(1991).

RL EMBL: X54613; CAA38455.1; -.

DR 5
 FT NON_TER 5 AA; 600 MW; 61E334DD6F00000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
 Db 2 A 2

RESULT 4

P83308 PRELIMINARY; PRT; 5 AA.

AC P83308;
 DT 01-JUN-2002 (TREMBLrel. 21; Created)

DT 01-JUN-2002 (TREMBLrel. 21; Last sequence update)

DE FMRFamide-like neuropeptide (LPRF-amide).

OS *Galus gallus* (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;

Archosauria; Amniota; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

OS [1]

SEQUENCE, AND SYNTHESIS.

RP

RC TISSUE=Brain;
 RX PubMed=613771;
 RA Dockray G.J.; Reeve J.R. Jr.; Shively J.; Gayton R.J.; Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide.";
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.

KW Neuropeptide;
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 0.0%; Score 0; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
 Db 1 L 1

RESULT 5

PB2181 PRELIMINARY; PRT; 6 AA.

AC P82181; PRELIMINARY;
 DT 01-JUN-2000 (TREMBLrel. 14; Created)

DT 01-JUN-2000 (TREMBLrel. 14; Last sequence update)

DE Chloroplast 50S ribosomal protein L10 beta (Fragment).

OS *Spinacia oleracea* (Spinach).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.

CC -!- SIMILARITY: BELONGS TO THE L10 FAMILY OF RIBOSOMAL PROTEINS.

RA InterPro; IPR01790; Ribosomal L10.

RL InterPro; IPR02363; Ribosomal L10.

DR Pfam; PF000466; Ribosomal L10; PARTIAL.

DR PROSITE; PS01109; RIBOSOMAL L10; PARTIAL.

DR Ribosomal protein; Chloroplast.

KW RNA-binding.

FT NON_TER 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 6;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
 Db 1 A 1

RESULT 6

P82541 PRELIMINARY; PRT; 6 AA.

AC P82541; PRELIMINARY;

DT 01-OCT-2000 (TREMBLrel. 15; Created)

DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)

DE Chloroplast 30S ribosomal protein S19 beta (Fragment).

OS *Spinacia oleracea* (Spinach).

PA	(ATHB-) ATHENA NEUROSCIENCES INC.	PI	Pleiss MA, Thorsett ED, Yednock TA;
XX		XX	WPI; 1996-097452/10.
PI	Pleiss MA, Thorsett ED, Yednock TA;	XX	
XX		XX	WPI; 1996-097452/10.
DR	New peptide(s) that bind VLA-4, inhibit leucocyte adhesion - useful esp. for treatment of inflammatory disease, e.g. multiple sclerosis	PT	New peptide(s) that bind VLA-4, inhibit leucocyte adhesion - useful esp. for treatment of inflammatory disease, e.g. multiple sclerosis
XX		PT	
PT	PT	PT	PT for treatment of inflammatory disease, e.g. multiple sclerosis
XX		XX	
PS	Example 9; Page 29; 42pp; English.	PS	Example 9; Page 29; 42pp; English.
XX		XX	
CC	AAR92598-R92659 represents VLA-4 binding peptides derived from the peptides shown in AAR92536-R92555 and AAR92563-R92594. VLA-4 is also known as alpha4beta1 integrin and CD49d/CD29. VLA-4 binds to the non-matrix molecule VCAM-1, which is expressed by endothelial and other cells. These sequences mimic short consensus sequences in the complementarity determining region 3 of antibody 21/6, and the FGN region of VCAM-1. These sequences inhibit the adhesion of leucocytes mediated by VLA-4. It is useful for treating inflammatory brain disorders (especially multiple sclerosis), meningitis, encephalitis, asthma, Alzheimer's disease, atherosclerosis, AIDS dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, tumour metastases and myocardial ischaemia. These sequences can also be labelled, and can then be used for in vivo or in vitro diagnosis, such as monitoring inflammatory responses, isolating leucocytes, in assays for inhibitors of VLA-4/VCAM-1 interactions and imaging sites of inflammation.	CC	AAR92598-R92659 represents VLA-4 binding peptides derived from the peptides shown in AAR92536-R92555 and AAR92563-R92594. VLA-4 is also known as alpha4beta1 integrin and CD49d/CD29. VLA-4 binds to the non-matrix molecule VCAM-1, which is expressed by endothelial and other cells. These sequences mimic short consensus sequences in the complementarity determining region 3 of antibody 21/6, and the FGN region of VCAM-1. These sequences inhibit the adhesion of leucocytes mediated by VLA-4. It is useful for treating inflammatory brain disorders (especially multiple sclerosis), meningitis, encephalitis, asthma, Alzheimer's disease, atherosclerosis, AIDS dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, tumour metastases and myocardial ischaemia. These sequences can also be labelled, and can then be used for in vivo or in vitro diagnosis, such as monitoring inflammatory responses, isolating leucocytes, in assays for inhibitors of VLA-4/VCAM-1 interactions and imaging sites of inflammation.
XX		XX	
CC	Query Match Score 21; DB 17; Length 5;	CC	Query Match Score 21; DB 17; Length 5;
CC	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	CC	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
CC	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	8 PVSF 11	Qy	8 PVSF 11
Db	1 PVSF 4	Db	2 PVSF 5
XX		XX	
RESULT 3		RESULT 3	
ID	AAR92604 standard; peptide; 6 AA.	ID	AAR92604 standard; peptide; 6 AA.
XX		XX	
AC	AAR92604;	AC	AAR92604;
XX		XX	
DT	10-SEP-1996 (first entry)	DT	10-SEP-1996 (first entry)
XX		XX	
DE	VLA-4 binding peptide #64.	DE	VLA-4 binding peptide #64.
XX		XX	
XX	VLA-4 binding peptide #67.	XX	VLA-4, inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR; alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis; complementarity determining region; inflammatory brain disorder; therapy; multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis; AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases; rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.
XX		XX	
XX	10-SEP-1996 (first entry)	XX	10-SEP-1996 (first entry)
XX		XX	
XX	VLA-4 binding peptide #67.	XX	VLA-4, inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR; alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis; complementarity determining region; inflammatory brain disorder; therapy; multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis; AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases; rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.
XX		XX	
OS	Synthetic.	OS	Synthetic.
XX		XX	
PH	Key	PH	Key
FT	Modified-site	FT	Modified-site
XX	1	XX	1
FT	/note= "acetylated"	FT	/note= "acetylated"
XX		XX	
PN	W09601644-A1.	PN	W09601644-A1.
XX		XX	
PD	25-JAN-1996.	PD	10-JUL-1995;
XX		XX	
PF	10-JUL-1995;	PF	06-JUN-1995;
XX		XX	
PR	95US-0467580.	PR	95US-0467580.
XX		XX	
PR	06-JUN-1995;	PR	11-JUL-1994;
PR	94US-0273055.	PR	94US-0273055.
XX		XX	
PA	(ATHB-) ATHENA NEUROSCIENCES INC.	PA	(ATHB-) ATHENA NEUROSCIENCES INC.
XX		XX	
PA	Pleiss MA, Thorsett ED, Yednock TA;	PA	Pleiss MA, Thorsett ED, Yednock TA;
XX		XX	

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 M protein - protein search, using sw model
 run on: November 21, 2003, 15:21:54 ; Search time 3.39041 Seconds
 (without alignments)
 224.632 Million cell updates/sec

title: US-09-010-377-5
 effect score: 35
 sequence: 1 XXXXXXXXPSFXXXXXX 1.8
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Databases : Issued Patents NA:
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	60.0	4	3	US-08-467-580-82	Sequence 82, Appl
2	21	60.0	4	5	PCT-US95-08516-82	Sequence 82, Appl
3	21	60.0	5	3	US-08-467-580-75	Sequence 75, Appl
4	21	60.0	5	5	PCT-US95-08516-75	Sequence 75, Appl
5	21	60.0	6	3	US-08-467-580-72	Sequence 72, Appl
6	21	60.0	6	3	US-08-467-580-83	Sequence 83, Appl
7	21	60.0	6	5	PCT-US95-08516-72	Sequence 72, Appl
8	21	60.0	6	5	PCT-US95-08516-83	Sequence 83, Appl
9	21	60.0	7	3	US-08-467-580-67	Sequence 67, Appl
10	21	60.0	7	5	PCT-US95-08516-67	Sequence 67, Appl
11	21	60.0	8	3	US-08-467-580-70	Sequence 70, Appl
12	21	60.0	8	5	PCT-US95-08516-70	Sequence 70, Appl
13	21	60.0	9	3	US-08-467-580-79	Sequence 79, Appl
14	21	60.0	9	5	PCT-US95-08516-79	Sequence 79, Appl
15	21	60.0	10	3	US-08-467-580-66	Sequence 66, Appl
16	21	60.0	10	3	US-08-467-580-66	Sequence 66, Appl
17	21	60.0	10	3	US-08-467-580-87	Sequence 87, Appl
18	21	60.0	10	5	PCT-US95-08516-40	Sequence 40, Appl
19	21	60.0	10	5	PCT-US95-08516-66	Sequence 66, Appl
20	21	60.0	10	5	PCT-US95-08516-87	Sequence 87, Appl
21	21	60.0	11	3	US-08-467-580-69	Sequence 69, Appl
22	21	60.0	11	3	US-08-467-580-69	Sequence 30, Appl
23	21	60.0	11	5	PCT-US95-08516-30	Sequence 69, Appl
24	21	60.0	11	5	PCT-US95-08516-69	Sequence 69, Appl
25	21	60.0	18	3	US-08-100-414B-29	Sequence 29, Appl
26	21	60.0	18	3	US-09-303-323-29	Sequence 29, Appl
27	21	60.0	18	4	US-09-770-014-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
 US-08-467-580-82
 Sequence 82, Application US/08467580B
 Patent No. 6001809
 GENERAL INFORMATION:
 APPLICANT: Thorsett, Eugene D
 INVENTOR: Yednock, Theodore A
 PLEISS, Michael A
 TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
 FILE REFERENCE: 123-US-CIPI1
 CURRENT APPLICATION NUMBER: US/08467580B
 CURRENT FILING DATE: 1995-06-06
 EARLIER APPLICATION NUMBER: 08/273,055
 EARLIER FILING DATE: 1994-07-11
 NUMBER OF SEQ ID NOS: 163
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 82
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: MOD_RES
 NAME/KEY: (1)_RES
 LOCATION: (1)
 OTHER INFORMATION: ACETYLYATION

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Peptide
 OTHER INFORMATION: Derived from VCAM-1
 US-08-467-580-82

Query Match Similarity 60.0% ; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0% ; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVSF 11.
 Db 1 PVSF 4.

RESULT 2
 PCT-US95-08516-82
 Sequence 82, Application PC/TUS9508516
 GENERAL INFORMATION:
 APPLICANT: ATHENA NEUROSCIENCES, INC.
 TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
 NUMBER OF SEQUENCES: 157
 CORRESPONDENCE ADDRESS:
 ADDRESS: ATHENA NEUROSCIENCES, INC.
 STREET: 800 Gateway Blvd.
 CITY: South San Francisco
 STATE: CA

COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM: Floppy disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/08516
 FILING DATE: 10-JUL-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/273,055
 FILING DATE: 11-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MOOL, LESLIE A.
 REGISTRATION NUMBER: 37,047
 REFERENCE/DOCKET NUMBER: 002010-008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 877-0900
 TELEFAX: (415) 877-3620
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US95-08516-82

Query Match 60.0%; Score 21; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 8 PVSF 11
 Db 1 PVSF 4

RESULT 3
 US-08-467-580-75
 Sequence 75, Application US/08467580B
 ; Patent No. 6001809
 GENERAL INFORMATION:
 ; APPLICANT: Thorsett, Eugene D
 ; APPLICANT: Pleiss, Michael A
 ; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
 ; FILE REFERENCE: 123-US-CIPI
 ; CURRENT FILING DATE: 1995-06-06
 ; EARLIER APPLICATION NUMBER: US/08/467,580B
 ; EARLIER FILING DATE: 1994-07-11
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 75
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: MOD_RES
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: ACETYLATION
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide
 ; OTHER INFORMATION: Derived from VCAM-1
 US-08-467-580-75

Query Match 60.0%; Score 21; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 8 PVSF 11
 Db 2 PVSF 5

RESULT 4
 PCT-US95-08516-75
 Sequence 75, Application PC/US9508516
 ; GENERAL INFORMATION:
 ; APPLICANT: ATHENA NEUROSCIENCES, INC.
 ; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
 ; NUMBER OF SEQUENCES: 157
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
 ; STREET: 800 Gateway Blvd.
 ; CITY: South San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/08516
 ; FILING DATE: 10-JUL-1995
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/273,055
 ; FILING DATE: 11-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MOOL, LESLIE A.
 ; REGISTRATION NUMBER: 37,047
 ; REFERENCE/DOCKET NUMBER: 002010-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 877-0900
 ; TELEFAX: (415) 877-3620
 ; INFORMATION FOR SEQ ID NO: 75:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 PCT-US95-08516-75

Query Match 60.0%; Score 21; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 8 PVSF 11
 Db 2 PVSF 5

RESULT 5
 US-08-467-580-72
 Sequence 72, Application US/08467580B
 ; GENERAL INFORMATION:
 ; APPLICANT: Thorsett, Eugene D
 ; PATENT NO. 6001809
 ; APPLICANT: Yednock, Theodore A
 ; APPLICANT: Pleiss, Michael A
 ; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
 ; FILE REFERENCE: 123-US-CIPI
 ; CURRENT FILING DATE: 1995-06-06
 ; EARLIER APPLICATION NUMBER: US/08/467,580B
 ; EARLIER FILING DATE: 1994-07-11
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 72
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

Result No.	Score	Query	Match	Length	DB	ID	Description	%
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2	21	60.0	12	12	US-09-910-831C-103		Sequence 103, App	
3	21	60.0	13	14	US-10-010-310-3		Sequence 3, Appl	
4	21	60.0	13	14	US-10-010-310-6		Sequence 6, Appl	
5	21	60.0	14	10	US-09-902-172-88		Sequence 88, Appl	
6	21	60.0	14	10	US-09-902-172-224		Sequence 224, App	
7	21	60.0	14	11	US-09-800-748-3064		Sequence 3064, App	
8	21	60.0	18	11	US-09-747-802-65		Sequence 65, Appl	
9	21	60.0	18	11	US-09-885-294-58		Sequence 58, Appl	
10	21	60.0	25	15	US-10-032-750-57		Sequence 57, Appl	
11	21	60.0	27	11	US-09-744-891-4315		Sequence 4315, App	
12	21	60.0	32	9	US-09-864-761-34806		Sequence 34806, A	
13	21	60.0	32	9	US-09-864-761-38915		Sequence 38915, A	
14	21	60.0	33	15	US-10-144-929-92		Sequence 92, Appl	
15	21	60.0	35	10	US-09-764-877-1329		Sequence 1329, Ap	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1	US-10-062-710-100	SEQUENCE 100, Application US/10062710
		; General Information:
		; Applicant: Li, Frank Q.
		; Inventor: Chu, Yong-Liang
		; Publication No. US20030049253A1
		; Title of Invention: Polymeric Conjugates for Delivery of MHC-Recognized Epitopes
		; Title of Invention: MHC-Recognized Epitopes
		; Title of Invention: Via Peptide Vaccines
		; File Reference: 3771-001-27
		; Current Application Number: US/10/062710
		; Prior Application Number: US 2002-02-05
		; Prior Filing Date: 2001-08-08
		; Software: FASTSEQ for Windows Version 4.0
		; SEQ ID NO 100
		; LENGTH: 11
		; TYPE: PRT
		; ORGANISM: Artificial Sequence
		; FEATURE: OTHER INFORMATION: HIV CTL-Epitopes
		US-10-062-710-100

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 2	US-09-390-832C-103	SEQUENCE 103, Application US/0990832C
		; General Information:
		; Applicant: Li, Frank Q.
		; Inventor: Chu, Yong-Liang
		; Publication No. US20030049253A1
		; Title of Invention: Polymeric Conjugates for Delivery of MHC-Recognized Epitopes
		; Title of Invention: MHC-Recognized Epitopes
		; Title of Invention: Via Peptide Vaccines
		; File Reference: 3771-001-27
		; Current Application Number: US/10/062710
		; Prior Application Number: US 60/310,498
		; Prior Filing Date: 2001-08-08
		; Software: FASTSEQ for Windows Version 4.0
		; SEQ ID NO 100
		; LENGTH: 11
		; TYPE: PRT
		; ORGANISM: Artificial Sequence
		; FEATURE: OTHER INFORMATION: HIV CTL-Epitopes
		US-10-062-710-100

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; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting Peptides
; FILE REFERENCE: PC/MC/JM/P1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-103

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Best Local Similarity 100.0%;  Pred. No. 1.e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   8  PVSF 11
Db   6  PVSF 9

RESULT 3
US-10-010-310-3
; Sequence 3, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; TITLE OF INVENTION: SEQUENCE AT THE SITE OF INTERACTION
; FILE REFERENCE: 112418.122
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-310-3

Query Match      60.0%;  Score 21;  DB 14;  Length 13;
Best Local Similarity 100.0%;  Pred. No. 1.e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   8  PVSF 11
Db   6  PVSF 9

RESULT 4
US-10-010-310-6
; Sequence 6, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; TITLE OF INVENTION: SEQUENCE AT THE SITE OF INTERACTION
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Computer generated synthetic peptide
US-10-010-310-6

Query Match      60.0%;  Score 21;  DB 10;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 1.e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   8  PVSF 11
Db   6  PVSF 9

RESULT 5
US-09-982-172-88
; Sequence 88, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
; FILE REFERENCE: 01/2283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-88

Query Match      60.0%;  Score 21;  DB 10;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 1.e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   8  PVSF 11
Db   6  PVSF 9

RESULT 6
US-09-982-172-224
; Sequence 224, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
; FILE REFERENCE: 01/2283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 224
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-224

Query Match      60.0%;  Score 21;  DB 10;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 1.e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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RL J. Mol. Biol. 179:185-214 (1984).
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 CC EMBL; AP003130; BAB4173; 1; -.
 CC EMBL; AP004823; BAB9436; 1; -.
 CC EMBL; UC0069; AAC63352; 1; ALT_INIT.
 CC PIR; B89322; B89822.
 CC HAMAP; MF_00574; -; 1.
 CC InterPro; IPR000231; Ribosomal_L30e.
 CC DR InterPro; IPR004038; Ribosomal_L7A.
 CC DR InterPro; IPR004037; Ribosomal_L7Ae.
 CC PFAM; PF01248; Ribosomal_L7ae; 1.
 CC PROSITE; PS01098; RIBOSOMAL_L7AE; FALSE_NEG.
 CC Hypothetical protein; Ribosomal Protein; Complete proteome.
 CC KW SQ SEQUENCE 84 AA; 9446 MW; 46EDC013ED0290963 CRC64;
 CC DR Query Match 60.0%; Score 21; DB 1; Length 84;
 CC Best Local Similarity 100.0%; Prd. No. 91; Mismatches 0; Indels 0; Gaps 0;
 CC DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 CC RESULT 3
 CC RXL7_STAAM STANDARD; PRT; 84 AA.
 CC ID Q53602; Q99W63;
 CC AC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Putative ribosomal protein L7ae-like.
 CC GN SAV0544 OR SA0502 OR MW0199
 CC OS Staphylococcus aureus (strain N315),
 CC OS Staphylococcus aureus (strain MW2), and
 CC OS Staphylococcus aureus.
 CC OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 CC OX NCBI_TaxID:158878, 158879, 196620, 1280;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=MJU30 / ATCC 700699, and N315;
 CC RX MEDLINE=220440717; PubMed=1141846;
 CC RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 CC RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 CC RA Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,
 CC RA Mizutani T., Takaiishi N.K., Sawano T., Inoue R.-I., Kaito C.,
 CC RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 CC RA Kanehisa M., Yanashita A., Oshima K., Furukawa K., Furukawa C., Shiba T.,
 CC RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 CC RA "whole genome sequencing of meticillin-resistant Staphylococcus
 CC RA aureus";
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=MJU2;
 CC RX MEDLINE=220440717; PubMed=12044378;
 CC RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 CC RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 CC RA Yamamoto K., Hiramatsu K.;
 CC RA "Genome and virulence determinants of high virulence community-
 CC RT acquired MRA";
 CC RN Lancet 359:1819-1827 (2002).
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=NCTC 8325;
 CC RX MEDLINE=98241542; PubMed=9573165;
 CC RA Wada A., Watanabe H.;
 CC RT "Penicillin-binding protein 1 of Staphylococcus aureus is essential
 CC RT for growth.";
 CC RT J. Bacteriol. 180:2759-2765 (1998).
 CC -1- SIMILARITY: BELONGS TO THE L7AE FAMILY OF RIBOSOMAL PROTEINS.

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 CC EMBL; AP003130; BAB4173; 1; -.
 CC EMBL; AP004823; BAB9436; 1; -.
 CC EMBL; UC0069; AAC63352; 1; ALT_INIT.
 CC PIR; B89322; B89822.
 CC HAMAP; MF_00574; -; 1.
 CC DR InterPro; IPR000231; Ribosomal_L30e.
 CC DR InterPro; IPR004038; Ribosomal_L7A.
 CC DR InterPro; IPR004037; Ribosomal_L7Ae.
 CC DR PFAM; PF01248; Ribosomal_L7ae; 1.
 CC DR PROSITE; PS01098; RIBOSOMAL_L7AE; FALSE_NEG.
 CC DR Hypothetical protein; Ribosomal Protein; Complete proteome.
 CC KW SQ SEQUENCE 84 AA; 9446 MW; 46EDC013ED0290963 CRC64;
 CC DR Query Match 60.0%; Score 21; DB 1; Length 84;
 CC Best Local Similarity 100.0%; Prd. No. 91; Mismatches 0; Indels 0; Gaps 0;
 CC DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 CC RESULT 4
 CC Y353_METUA STANDARD; PRT;
 CC ID Y353_METUA STANDARD; PRT;
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 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Hypothetical protein MJ0353.
 CC GN MJ0353.
 CC OS Methanococcus jannaschii
 CC OC Archaea; Euryarchaeota; Methanococcales;
 CC OC Methanocaldococcaceae; Methanococcaceae;
 CC NCBI TaxID:2103;
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 CC RC BUILT C.J., White O., Olsen G.J., Fleischmann R.D., Clayton R.A., Kerlavage A.R., Dougherty E.P., Weinstock K.G., Merrick J.M., Sutton G.G., Blake J.A., Fitzgerald L.M., Overbeek R., Kirkness E.P., Weidman J.F., Sutton G.J., Geethagen N.S.M., Weidman J.F., Utterback T.R., Kelley J.M., Sadow P.W., Scott J.L., Fuerst M.A., Kaine B.P., Borodovsky M., Cottontail M.D., Roberts K.M., Hurst M.A., Kline H.-P., Fraser C.M., Klenk H.-P., Smith H.O., Woese C.R., Venter J.C., RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii";
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 CC EMBL; U67488; AAB98342; 1; -.
 CC DR PIR; A64344; A64344.
 CC DR TIGR; MJ0353; -.
 CC KW Hypothetical protein; Complete proteome.

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DM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:39 ; Search time 7.76712 Seconds

(without alignments)
598.027 Million cell updates/sec

Title: US-09-010-377-5
Perfect score: 35

Sequence: 1 XXXXXXXXPPSFXXXXXX 1.8

Scoring table: BLASTM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Literals first 45 summaries

Database : SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_protein:*

12: sp_virus:*

13: sp_vertbrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriip:*

17: sp_archeap:*

18: sp_bacteria:*

19: sp_fungi:*

20: sp_human:*

21: sp_invertebrate:*

22: sp_mammal:*

23: sp_mhc:*

24: sp_organelle:*

25: sp_phage:*

26: sp_plant:*

27: sp_protein:*

28: sp_virus:*

29: sp_vertbrate:*

30: sp_unclassified:*

31: sp_rvirus:*

32: sp_bacteriip:*

33: sp_archeap:*

34: sp_bacteria:*

35: sp_fungi:*

36: sp_human:*

37: sp_invertebrate:*

38: sp_mammal:*

39: sp_mhc:*

40: sp_organelle:*

41: sp_phage:*

42: sp_plant:*

43: sp_protein:*

44: sp_virus:*

45: sp_vertbrate:*

46: sp_unclassified:*

47: sp_rvirus:*

48: sp_bacteriip:*

49: sp_archeap:*

50: sp_bacteria:*

51: sp_fungi:*

52: sp_human:*

53: sp_invertebrate:*

54: sp_mammal:*

55: sp_mhc:*

56: sp_organelle:*

57: sp_phage:*

58: sp_plant:*

59: sp_protein:*

60: sp_virus:*

61: sp_vertbrate:*

62: sp_unclassified:*

63: sp_rvirus:*

64: sp_bacteriip:*

65: sp_archeap:*

66: sp_bacteria:*

67: sp_fungi:*

68: sp_human:*

69: sp_invertebrate:*

70: sp_mammal:*

71: sp_mhc:*

72: sp_organelle:*

73: sp_phage:*

74: sp_plant:*

75: sp_protein:*

76: sp_virus:*

77: sp_vertbrate:*

78: sp_unclassified:*

79: sp_rvirus:*

80: sp_bacteriip:*

81: sp_archeap:*

82: sp_bacteria:*

83: sp_fungi:*

84: sp_human:*

85: sp_invertebrate:*

86: sp_mammal:*

87: sp_mhc:*

88: sp_organelle:*

89: sp_phage:*

90: sp_plant:*

91: sp_protein:*

92: sp_virus:*

93: sp_vertbrate:*

94: sp_unclassified:*

95: sp_rvirus:*

96: sp_bacteriip:*

97: sp_archeap:*

98: sp_bacteria:*

99: sp_fungi:*

100: sp_human:*

101: sp_invertebrate:*

102: sp_mammal:*

103: sp_mhc:*

104: sp_organelle:*

105: sp_phage:*

106: sp_plant:*

107: sp_protein:*

108: sp_virus:*

109: sp_vertbrate:*

110: sp_unclassified:*

111: sp_rvirus:*

112: sp_bacteriip:*

113: sp_archeap:*

114: sp_bacteria:*

115: sp_fungi:*

116: sp_human:*

117: sp_invertebrate:*

118: sp_mammal:*

119: sp_mhc:*

120: sp_organelle:*

121: sp_phage:*

122: sp_plant:*

123: sp_protein:*

124: sp_virus:*

125: sp_vertbrate:*

126: sp_unclassified:*

127: sp_rvirus:*

128: sp_bacteriip:*

129: sp_archeap:*

130: sp_bacteria:*

131: sp_fungi:*

132: sp_human:*

133: sp_invertebrate:*

134: sp_mammal:*

135: sp_mhc:*

136: sp_organelle:*

137: sp_phage:*

138: sp_plant:*

139: sp_protein:*

140: sp_virus:*

141: sp_vertbrate:*

142: sp_unclassified:*

143: sp_rvirus:*

144: sp_bacteriip:*

145: sp_archeap:*

146: sp_bacteria:*

147: sp_fungi:*

148: sp_human:*

149: sp_invertebrate:*

150: sp_mammal:*

151: sp_mhc:*

152: sp_organelle:*

153: sp_phage:*

154: sp_plant:*

155: sp_protein:*

156: sp_virus:*

157: sp_vertbrate:*

158: sp_unclassified:*

159: sp_rvirus:*

160: sp_bacteriip:*

161: sp_archeap:*

162: sp_bacteria:*

163: sp_fungi:*

164: sp_human:*

165: sp_invertebrate:*

166: sp_mammal:*

167: sp_mhc:*

168: sp_organelle:*

169: sp_phage:*

170: sp_plant:*

171: sp_protein:*

172: sp_virus:*

173: sp_vertbrate:*

174: sp_unclassified:*

175: sp_rvirus:*

176: sp_bacteriip:*

177: sp_archeap:*

178: sp_bacteria:*

179: sp_fungi:*

180: sp_human:*

181: sp_invertebrate:*

182: sp_mammal:*

183: sp_mhc:*

184: sp_organelle:*

185: sp_phage:*

186: sp_plant:*

187: sp_protein:*

188: sp_virus:*

189: sp_vertbrate:*

190: sp_unclassified:*

191: sp_rvirus:*

192: sp_bacteriip:*

193: sp_archeap:*

194: sp_bacteria:*

195: sp_fungi:*

196: sp_human:*

197: sp_invertebrate:*

198: sp_mammal:*

199: sp_mhc:*

200: sp_organelle:*

201: sp_phage:*

202: sp_plant:*

203: sp_protein:*

204: sp_virus:*

205: sp_vertbrate:*

206: sp_unclassified:*

207: sp_rvirus:*

208: sp_bacteriip:*

209: sp_archeap:*

210: sp_bacteria:*

211: sp_fungi:*

212: sp_human:*

213: sp_invertebrate:*

214: sp_mammal:*

215: sp_mhc:*

216: sp_organelle:*

217: sp_phage:*

218: sp_plant:*

219: sp_protein:*

220: sp_virus:*

221: sp_vertbrate:*

222: sp_unclassified:*

223: sp_rvirus:*

224: sp_bacteriip:*

225: sp_archeap:*

226: sp_bacteria:*

227: sp_fungi:*

228: sp_human:*

229: sp_invertebrate:*

230: sp_mammal:*

231: sp_mhc:*

232: sp_organelle:*

233: sp_phage:*

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235: sp_protein:*

236: sp_virus:*

237: sp_vertbrate:*

238: sp_unclassified:*

239: sp_rvirus:*

240: sp_bacteriip:*

241: sp_archeap:*

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N Neisseria meningitidis (serogroup B).
S Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
C Neisseriaceae; Neisseria.
N NCBI_TaxID=49;
N
N [1]
N
N SEQUENCE FROM N.A.
N
N STRAIN=M658 / Serogroup B;
N MEDLINE=20175755; PubMed=10710307;
N Tettelin H.; Saunders N.J.; Heidelberg J.; Jeffries A.C.; Nelson K.E. ;
N Eisen J.A.; Ketchum K.A.; Hood D.W.; Peden J.F.; Dodson R.J. ;
N Nelson W.C.; Gwinn M.L.; DeBoy R.; Peterson J.D.; Hickey E.K. ;
N Haft D.H.; Salzberg S.L.; White O.; Fleischmann R.D.; Dougherty B.A. ;
N Mason T.; Ciecko A.; Parksey D.S.; Blair B.; Cittone H.; Clark E.B. ;
N Cotton M.D.; Utterback T.R.; Khouri H.; Olin H.; Vamathevan J. ;
N Gill J.; Sczarlato V.; Masiognani V.; Pizzola M.; Grandi G.; Sun L. ;
N Smith H.O.; Fraser C.M.; Moxon E.R.; Rappuoli R.; Venter J.C. ;
N "Complete genome sequence of Neisseria meningitidis serogroup B strain
N MC58. ";
N MC58. ";
N
N Science 287:1809-1815 (2000).
N EMBL; AE002416; AAF41040.1; -.
N TIGR; NM00613; -.
N Hypothetical protein; Complete proteome.
N
N SEQUENCE 35 AA; 4022 MW; A3677246569B6306 CRC64;
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N Query Match 60.0%; Score 21; DB 16; Length 35;
N Best Local Similarity 100.0%; Pred. No. 2.1e+02;
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N Y 8 PVSF 11
N Y ||||| |
N b 21 PVSF 24
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N RESULT 3
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N BBED2D Q8EYD2 PRELIMINARY; PRT; 36 AA.
N
N Q8EYD2; PRELIMINARY; PRT; 36 AA.
N
N STRAIN=5601 / Serogroup Icterohaemorrhagiae / Serovar Jai;
N Ren S.; Created)
N 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
N Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
N
N TITI 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
N TITI 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
N HYPOTHETICAL PROTEIN
N LAA284.
N
N Leptospira interrogans.
N Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
N NCBI_TaxID=173;
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N STRAIN=5601 / Serogroup Icterohaemorrhagiae / Serovar Jai;
N Ren S.; Created)
N Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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N TITI 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
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N LAA284.
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N Y ||||| |
N b 21 PVSF 24
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N RESULT 4
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N Q8FH25; PRELIMINARY; PRT; 42 AA.
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N 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
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N C2108.
N Escherichia coli O6.
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